PATENT DOCKET 709

IN THE UNITED STATES PATENT AND TRADEMARK OFFICE

In re Application of	)	Group Art Unit: 1806
Paul J. Carter et al.	)	Examiner: L. FEISEE
Serial No. 07/715272	)	
Filed: June 14, 1991	)	
For: Immunoglobulin Variants	)	460 Point San Bruno Boulevard South San Francisco, CA 94080

#20
Amd
9-30-93

DECLARATION OF ROBERT F. KELLEY PURSUANT TO 37 CFR §1.132

Honorable Commissioner of Patents
and Trademarks
Washington, D.C. 20231

Sir:

I, ROBERT F. KELLEY, do hereby declare as follows:

1. I received my Ph.D. in Biochemistry in 1984 from the University of Iowa. Following my Ph.D, I was a NIH postdoctoral fellow in the Department of Molecular Biophysics & Biochemistry at Yale University from July 1984 to December 1985. In 1986, I joined the Biocatalysis Department at Genentech, Inc. as an Associate Scientist. In September 1988, I was promoted to Scientist and I am employed in that capacity at present. (The Biocatalysis Department has been renamed "Protein Engineering"). I am the author or co-author of 22 publications relating to the 3-D structures and folding of various proteins. A copy of my curriculum vitae is attached as Exhibit "A".

2. I understand that the Patent Office has rejected the above application on the basis that the application as filed does not provide sufficient disclosure to enable a skilled biochemist to carry out the method of claim 1 because the Examiner believes no clear guidance exists in the specification to allow a skilled biochemist to make the "consensus human variable domain" and substitute an import (i.e. non-human) Complementary Determining Region (CDR) amino acid sequence for the corresponding human CDR amino acid sequence, as set forth in claim 1. I further understand that the Office considers that

the only guidance in the specification with regards to the substitutions is the amino acid sequences of SEQ ID NO: 3 and 4.

3. I have read the above application, the Office Action date May 19, 1992 (Paper # 17) rejecting the claims of the application, and the proposed amendment of the claims in response to the rejection. In my opinion, the skilled biochemist could have readily carried out the method of claim 1 in order to make a humanized antibody, using the general knowledge available in the field on and before June 14, 1991, and the information given in the above application. The bases for my opinion are given in paragraphs 4 to 7 below.

4. Claim 1 relates to a method of making a humanized antibody. Steps a and b of claim 1, as amended, discuss identification of the CDR amino acid sequences of a non-human import antibody (to be humanized) and a consensus human variable domain of a human immunoglobulin subgroup. The consensus human variable domain constitutes an amino acid sequence comprising the most commonly occurring amino acids at each position in the variable domain of a particular human immunoglobulin subgroup as defined by Kabat *et al.*, *Sequences of Proteins of Immunological Interest*, Fourth Edition, U.S. Dept. of Health & Human Services, pubs., (1987), a copy of which is attached as Exhibit "B". The immunoglobulin subgroups referred to in Kabat *et al.* were grouped according to the amino acid sequence homology between human immunoglobulin *variable* domains, and the most commonly occurring amino acids at each position in the variable domain for each subgroup were identified (i.e. the "consensus human variable domain"). The skilled biochemist could have used the consensus human variable domains of the light chain and heavy chain subgroups having the greatest number of sequences (i.e. light chains kappa subgroup I and heavy chains subgroup III) as disclosed in Kabat *et al.* (see page 17, first paragraph of the specification) to humanize the non-human antibody of interest. Alternatively, the skilled biochemist could have chosen the consensus human variable domain of another human immunoglobulin subgroup as defined in Kabat *et al.* (i.e. the consensus human variable domain for human kappa light chains subgroups II to IV, human lambda light chains subgroups I to VI, or human

heavy chains subgroups I or II [see pages 41-76 and 160-167 of Kabat *et al.*]). Therefore, the skilled biochemist could have elected to use a consensus human variable domain other than those defined as SEQ ID NO: 3 & 4 on page 17 of the above application, as the consensus human variable domains for other subgroups were compiled in Kabat *et al.* Page ix of Kabat *et al.* identifies the residues forming the CDR regions of heavy and light chain variable domains tabulated from human and mouse variable domains. Kabat *et al.* have adopted standardized numbering for each of the residue locations. Accordingly, the skilled biochemist could have identified the CDR regions of the consensus human variable domain and the import variable domain using the teachings of Kabat *et al.* Alternatively, the structural definition of Chothia *et al.*, *J. Mol. Biol.*, **196:** 901-917 (1987) (see page 16, third paragraph of the specification) could have been adopted to identify the CDR regions of the consensus and import variable domains. Hence, it would have been straightforward for the skilled biochemist to carry out steps a and b of claim 1 using the information provided in the specification.

5. Step c of claim 1 discloses the step of replacing the corresponding human CDR sequence with the import CDR amino acid sequence. This step could have been carried out routinely by the skilled biochemist by manual tabulation or using a computer program such as the ALIGN program, (Dayhoff *et al.*, *Meth. Enzymol.*, **91**:524-545 [1983]) which was available prior to June 14, 1991. Steps a to c of claim 1 would have resulted in the characterization of a primary amino acid sequence encoding a humanized variable domain with import (non-human) CDR regions.

6. Steps d to g of claim 1 relate to the identification of Framework Region (FR) residues in the consensus human variable domain which are non-homologous to the corresponding import FR residues and replacement of such non-homologous human residues with corresponding import residues, if the residues are expected to have any one of the effects specified in step f. The locations of FR residues in human and mouse variable domains are indicated in Kabat *et al.* (see page ix) and the structural definition of the FR's was available (see Chothia *et al.*) Hence, it would have been straightforward for the skilled immunologist to identify the FR residues in the consensus human variable domain and the

import sequence. Using computer programs (such as the INSIGHT program [Biosym Technologies], available before June 14, 1991), the skilled biochemist would have been able to study the 3-dimensional structure of an antibody in order to establish whether a particular non-homologous import amino acid residue is likely to have one of the effects discussed in section f of claim 1. Information is provided on pages 14 to 16 of the specification which would have enabled the skilled biochemist to determine whether any non-homologous residue(s) would be expected to have the effects claimed. The techniques claimed in steps d to g of claim 1 could have been carried out routinely by a person versed in the relevant art, prior to June 14, 1991.

7. Steps a to g of claim 1 would have lead to the characterization of an amino acid sequence of a humanized antibody having non-human CDR amino acid residues and, optionally, having one or more non-human FR residues. In order to prepare the humanized antibody as claimed in claim 1, step h, the skilled biochemist could have synthesized the antibody using a peptide synthesizer which was commercially available before June 14, 1991. Alternatively, the antibody could have been made in recombinant cell culture (see page 26, last paragraph of the specification). Preparation of the antibody would have been straightforward to perform by the person skilled in the art, once the amino acid sequence of the humanized antibody had been characterized.

8. I understand that the Patent Office has rejected the above application on the basis that the sites in the variable domain referred to in claims 6, 7, and 9 are relevant to IgG antibodies only. It is my opinion that the sites referred to in claims 6, 7, and 9 would be relevant to other immunoglobulins. The basis for my opinion is given in paragraph 9 below.

9. The sites referred to in claims 6, 7, and 9 are the residue locations, or sites, of the FR residues in the heavy or light chain forming the variable domain of immunoglobulins. The residue sites referred to in claims 6, 7 & 9 relate to the position of a residue in the 3-D structure of the variable domain. Kabat *et al.* have used universal numbering for the amino acid residue locations of the variable domains for each of the immunoglobulin subgroups mentioned in the reference. The FR residue sites

indicated may be occupied by an amino acid residue which is non-homologous to the corresponding consensus human variable domain residue, and which is likely to have at least one of the effects discussed in step f of claim 1. These residue locations or sites are applicable *across species* (see page 16, line 8 of the specification). Accordingly, it is likely that an amino acid residue located at one of the sites indicated in claims 6, 7 and 9 will have one of the effects of claim 1 (step f), regardless of the antibody in which it is located, because it will be in the same position in the 3-D structure of the antibody variable domain as the residue sites referred to in the rejected claims. Accordingly, the examples of residue locations to be substituted in the variable domains would be applicable to antibodies, other than IgG antibodies.

10. I understand that the Patent Office has rejected the above application on the grounds that the invention as claimed is disclosed in Queen *et al.*, *Proc. Natl. Acad. Sci.*, **86**:10029-10033 (1989) or Co *et al.*, *Proc. Natl. Acad. Sci.*, **88**:2869-2873 (1991) and that the Office has suggested that the human variable domains disclosed in these references may have the same amino acid sequences as one of the consensus human variable domains disclosed in Kabat *et al.*

11. The above statements regarding the state of knowledge as of June 14, 1991, do not establish that the invention claimed in this application was known, or would have been obvious, to the skilled biochemist at the time the invention was made. To the contrary, after having read the citations relied upon by the Patent Office, it is my judgement that these documents would not have disclosed, nor suggested, the methods claimed. The basis for my opinion is given below.

12. The invention of the above application can be distinguished on the basis that a *consensus human variable domain* is used to "humanize" a non-human antibody of interest. The Queen *et al.* and Co *et al.* publications fail to disclose a consensus human variable domain. Instead, these publications refer to the use of a human variable domain having the closest sequence homology to the variable domain of the non-human antibody to be humanized. Queen *et al.* used the Eu human variable domain sequence (see Fig 2 thereof) and Co *et al.* used the variable domains of the Pom or Eu human

antibodies (see Fig 1 thereof). The sequences used in Queen *et al.* and Co *et al.* do not constitute a consensus human variable domain of a human immunoglobulin subgroup. The sequence identity between the amino acid sequences of the FR residues of the variable domains of the Pom or Eu heavy or light chains compared to the FR residues of the consensus human variable domains of each of the human immunoglobulin subgroups as defined by Kabat *et al.* is illustrated in Table 1 (see Exhibit "C", attached hereto). The CDR residues were not used in the comparison because of the large number of differences between these residues for variable domains of different antibodies. The Pom and Eu variable domain sequences were taken from Kabat *et al.* The consensus human variable domains of the V_L lambda subgroups IV and V were not compared, as these subgroups have too few members. While the variable domain of Eu is classified in subgroups V_L kappa I and V_H I, and the variable domain of Pom is classified in subgroups V_L kappa III and V_H III, it is apparent that the Eu and Pom variable domain amino acid sequences are not consensus human variable domains of any immunoglobulin subgroup. This is further demonstrated in the following paragraph.

13. Exhibits "D" and "C" attached hereto, show the differences in the amino acid sequences of the Pom and Eu heavy and light chain variable domains compared to the consensus human variable domain of the subgroup in which they are classified. Exhibit D illustrates an alignment of the amino acid sequences of the light chain variable domains of Eu, Pom and the consensus variable domain of the V_L kappa subgroup I (in which the light chain variable domain of Eu is classified). Exhibit E illustrates an alignment of the amino acid sequences of the heavy chain variable domains of Eu, Pom and the consensus variable domain of the V_H subgroup III (in which the heavy chain variable domain of Pom is classified). Even though Eu is classified in V_L kappa I, it has seven framework residues which are different from the framework residues of the kappa I consensus sequence. Furthermore, while Pom is classified in the V_H III subgroup, eight of its framework residues differ from the corresponding framework residues of the V_H III consensus sequence. There are, of course, many differences between the CDR residues of the consensus sequences and the corresponding CDR residues of Pom and Eu.

It is clear from the information in Exhibits C, D, & E that the Queen *et al.* and Co *et al.* publications fail to disclose a method wherein a non-human import antibody is humanized using a consensus human variable domain of an immunoglobulin subgroup.

14. I understand the Patent Office has rejected the above application on the basis that the invention claimed in claims 3 & 4 would have been obvious in light of Queen *et al.*, or Co *et al.*, when read in conjunction with Wallick *et al., J. Exp. Med.*, **168** (1988). After reading these references, it is my opinion that the invention claimed in claims 3 and 4 is novel and would not have been obvious in light of the citations. The basis for my opinion is given in the following paragraph.

15. Claim 1 of the above application relates to a method of using a consensus human variable domain to "humanize" a non-human antibody (e.g. muMAb4D5). Use of a consensus human variable domain from a human immunoglobulin subgroup to humanize a non-human antibody is not disclosed in Queen *et al.*, Co *et al.* or Wallick *et al.* Wallick *et al.* does not relate to a method of humanizing a non-human antibody, much less a method of humanizing a non-human antibody using a consensus human variable domain of a human immunoglobulin subgroup. The skilled biochemist would have had no motivation at the filing date of this application to use a consensus human variable domain to humanize a non-human antibody, because the techniques in the prior literature had all relied upon using a human variable domain sequence which has the closest sequence homology to the non-human variable sequence (to be humanized) in order to reduce the likelihood of introducing distortions into the CDR's (see column 2 on page 10031 of Queen *et al.*) or to "retain high binding affinity in the humanized antibodies" (see column 1 on page 2871 of Co *et al.*). The method claimed in the above application does not rely on a high degree of homology between the variable domain of the non-human sequence and the consensus variable domain which is used to humanize the non-human sequence. It was surprising that a consensus variable domain of a selected immunoglobulin subgroup could be used to humanize a non-human antibody, regardless of the degree of homology between the human and non-human amino acid sequences. It was also surprising that the humanized antibody so formed retained,

and in some instances, had increased antigen binding affinity compared to the non-human antibody from which it was derived. The above application shows that the huMAb4D5-8 variant actually binds the $p185^{HER2}$ ECD 3-fold more tightly than muMAb4D5 (see page 82 lines 31 & 32 to page 83, line 1 of the specification), which could not have been predicted by the ordinarily skilled biochemist at the time the specification was filed. Claim 3 refers to the step of finding any glycosylation site which is likely to affect the antigen binding or affinity in the import antibody and substituting the glycosylation site *into* the *consensus* amino acid sequence. Claim 4 refers to the step of *replacing* glycosylation sites of the consensus domain with the corresponding import amino acid residues if such glycosylation sites are not present in the import sequence. In my opinion, these claims would not have been obvious over the prior literature because the reference failed to disclose the use of a human consensus variable domain to humanize the non-human antibody. Accordingly, the skilled biochemist would have had no motivation to replace or insert glycosylation sites into a consensus amino acid sequence, as claimed in claims 3 and 4 of the application.

16. I declare further that all statements made herein of my own knowledge are true and that all statements made on information and belief are believed to be true; and further that these statements were made with the knowledge that willful false statements and the like so made are punishable by fine or imprisonment, or both, under section 1001 of Title 18 of the United States Code, and that such willful false statements may jeopardize the validity of the application or any patent issuing thereon.

Dated: 9/20/93 Signed: Robert F. Kelley
ROBERT F. KELLEY

CERTIFICATE OF MAILING

I hereby certify that this correspondence is being deposited with the United States Postal Service as first class mail in an envelope addressed to: Commissioner of Patents and Trademarks, Washington, D.C. 20231, on September 20, 1993.

Dated: September 20, 1993

Louise Strasbaugh
Louise Strasbaugh

w012.u

EXHIBIT A

Robert F. Kelley **CURRICULUM VITAE** **September, 1993**

Work address:

Genentech, Inc.
Protein Engineering Dept.
South San Francisco, CA 94080

Home address:

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San Bruno, CA 94066

Personal information:

Birthdate: November 7, 1957
Married, Wife's name: Wendy L. Kelley
One child: Brian F. Kelley

Education:

B.S., Biochemistry, Michigan State University, 1979
Ph. D., Biochemistry, University of Iowa, 1984

Employment positions:

Teaching assistant, Chemistry Dept., Michigan State Univ., 1978-1979
Teaching assistant, Biochemistry Dept., University of Iowa, 1979-1981
Graduate research assistant, Biochemistry Dept., University of Iowa, 1982-April 1984
Postdoctoral associate, Biochemistry Dept., University of Iowa, May 1984-June 1984
NIH postdoctoral fellow, Dept. of Molecular Biophysics & Biochemistry, Yale University, July 1984-Dec. 1985
Associate Scientist, Biocatalysis Dept., Genentech, Inc., January 1986-September 1988
Scientist, Biomolecular Chemistry Dept., Genentech, Inc., September 1988-present

Awards and membership in professional organizations:

Biophysical Society, 1983-present
American Chemical Society, 1991-present

Scientific publications

Kelley, R.F., & Stellwagen, E. (1984) "Conformational transitions of thioredoxin in guanidine hydrochloride", Biochemistry 23, 5095-5102.

Kelley, R.F., Wilson, J., Bryant, C., & Stellwagen, E. (1986)"Effects of guanidine hydrochloride on the refolding kinetics of denatured thioredoxin", Biochemistry 25, 728-732.

Wilson, J., Kelley, R.F., Shalongo, W., Lowery, D., & Stellwagen, E. (1986) "Equilibrium and kinetic measurements of the conformational transitionof thioredoxin in urea", Biochemistry 25, 7560-7566.

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Kelley, R.F., Shalongo, W., Jagannadham, M.V., & Stellwagen, E. (1987) "Equilibrium and kinetic measurements of the conformational transition of reduced thioredoxin", Biochemistry 26, 1406-1411.

Kelley, R.F., & Richards, F.M. (1987) "Replacement of proline 76 with alanine eliminates the slowest kinetic phase in thioredoxin folding",Biochemistry 26, 6765-6774.

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EXHIBIT C

TABLE 1
SEQUENCE IDENTITY - (%)

CONSENSUS VARIABLE DOMAIN SUBGROUP	EU	POM
V_L kappa I	92	76
V_L kappa II	61	71
V_L kappa III	72	85
V_L kappa IV	73	78
V_L lambda I	61	59
V_L lambda II	57	54
V_L lambda III	59	56
V_L lambda VI	52	49
V_H I	83	64
V_H II	53	62
V_H III	61	91

EXHIBIT D

Variable Light Domain

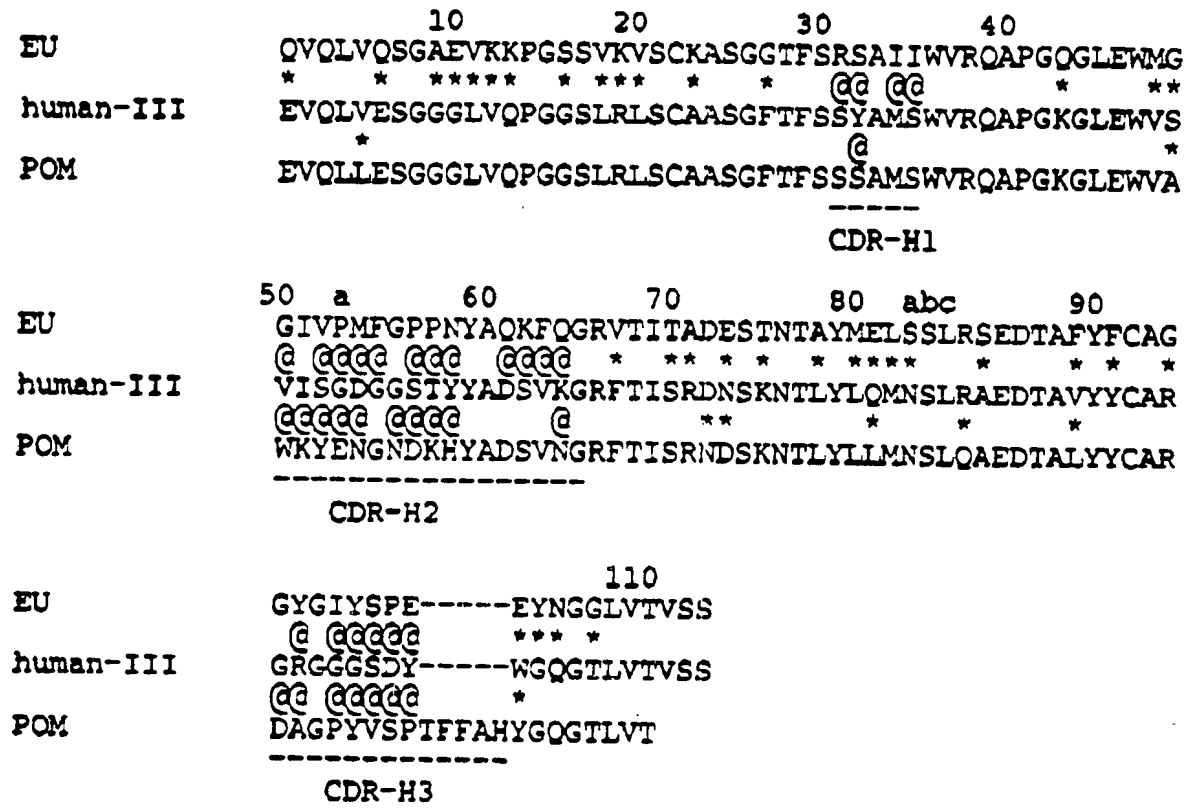
```
                  10        20        30        40
EU          DIQMTQSPSTLSASVGDRVTITCRASQ-SINTWLAWYQQKPGKAPKLLMY
                    *                 @ @@@                 *
Kappa-I     DIQMTQSPSSLSASVGDRVTITCRASQ--ISNYLAWYQQKPGKAPKLLIY
            * *     **  * * * * **     @@@@@          *** *
POM         EIVMTQSPVTLSVSPGERATLSCRASQSISNSYLAWYQQKPSGSPRLLIY
                                      ----------
                                      CDR-L1

           50        60        70        80        90        100
EU          KASSLESGVPSRFIGSGSGTEFTLTISSLQPDDFATYYCQQYNSDSKMFGQ
            @           *         *         *           @@@@
Kappa-I     AASSLESGVPSRFSGSGSGTDFTLTISSLQPEDFATYYCQQYNSLPWTFGQ
            @  @@@@ * *           *         *     *     @@ @
POM         GASTRATGIPARFSGSGSGTEFTLTISSLQSEDFAVYYCQQYNNWPPTFGQ
            -------                                 ----------
            CDR-L2                                  CDR-L3

EU          GTKVEVKGT
                  * *
Kappa-I     GTKVEIKRT
                *
POM         GTRVEIKR
```

KEY: * = differences in FR residues

@ = differences in CDR residues

EXHIBIT E

Variable Heavy Domain



KEY: * = differences in FR residues

@ = differences in CDR residues

Byeon, I.-J.L., Kelley, R.F., & Llinas, M. (1989) "^{1}H-NMR structural characterization of a recombinant kringle-2 domain from human tissue-type plasminogen activator", Biochemistry 28, 9350-9360.

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Carter, P., Kelley, R.F., Rodrigues, M.L., Snedecor, B.R., Covarrubias, M., Velligan, M.D., Wong, W.-L. T, Rowland, A.M., Kotts, C.E., Carver, M.E., Yang, M., Bourell, J.H., Shepard, H.M., & Henner, D.J. (1992) "High level Escherichia coli expression and production of a bivalent humanized antibody fragment" Bio/Technology, 10, 163-167.

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Kelley, R.F., O'Connell, M.P., Carter, P., Presta, L., Eigenbrot, C., Covarrubias, M., Snedecor, B., Speckart, R., Blank, G., Vetterlein, D., & Kotts, C. (1993) "Characterization of humanized anti-p185^{HER2} antibody Fab fragments produced in *E. coli*" ACS Symposium Series No. 526, *Protein Folding: In Vivo and In Vitro*, J.L. Cleland & J. King, eds., pp. 218-239.

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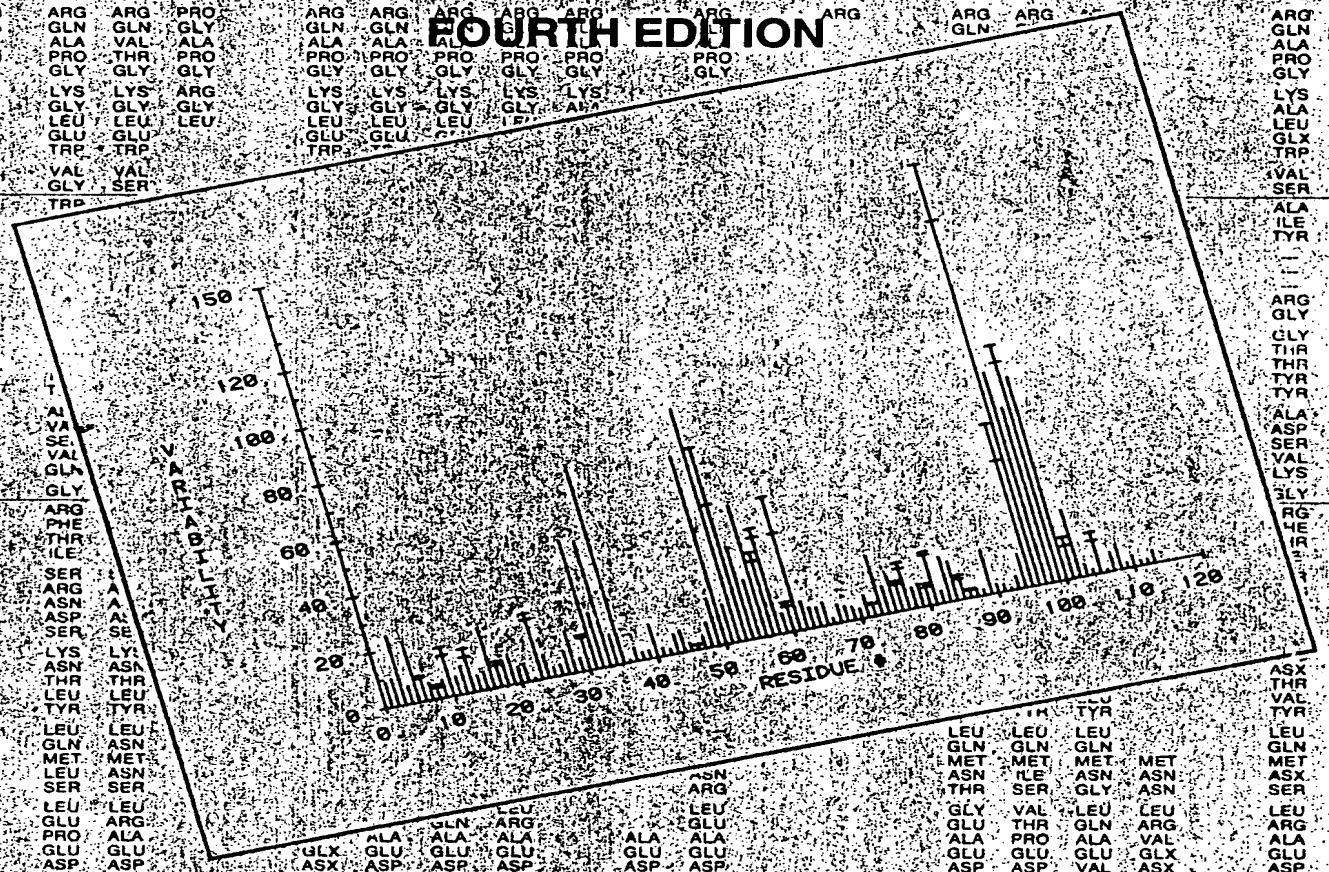
Bethesda, Maryland

Exhibit B

SEQUENCES OF PROTEINS OF IMMUNOLOGICAL INTEREST

FOURTH EDITION



1987

U.S. DEPARTMENT OF HEALTH AND HUMAN SERVICES
Public Health Service
National Institutes of Health

SEQUENCES OF PROTEINS OF IMMUNOLOGICAL INTEREST

FOURTH EDITION

Tabulation and Analysis of
Amino Acid and Nucleic Acid Sequences of
Precursors, V-Regions, C-Regions, J-Chain,
T-Cell Receptor for Antigen, T-Cell Surface Antigens,
β_2-Microglobulins, Major Histocompatibility Antigens,
Thy-1, Complement, C-Reactive Protein, Thymopoietin,
Post-gamma Globulin, and α_2-Macroglobulin

1987

Elvin A. Kabat, Tai Te Wu †, Margaret Reid-Miller ‡,*
Harold M. Perry ‡, and Kay S. Gottesman ‡

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The collection and maintenance of this data base is sponsored through Contract N01-RR-8-2158 by the following components of the National Institutes of Health, Bethesda, MD 20892:

Division of Research Resources
National Cancer Institute
National Institute of Allergy and Infectious Diseases
National Institute of Arthritis, Diabetes, Digestive and Kidney Diseases
National Institute of General Medical Sciences

U.S. DEPARTMENT OF HEALTH
AND HUMAN SERVICES
Public Health Service
National Institutes of Health
(1987)

TABLE OF CONTENTS

considered uncertain by the authors have not been included in the table. In some instances the symbol # is used to indicate that several amino acid residues were found in one position, and these residues are listed in the notes. The four columns at the end of each table give:

1. the number of residues sequenced at that position,
2. the number of different amino acids found at that position,
3. the number of times the most common amino acid occurred and that amino acid in parentheses, and
4. the variability.

Variability is calculated (11) as:

$$\text{Variability} = \frac{\text{Number of different amino acids occurring at a given position}}{\text{Frequency of the most common amino acid at that position}}$$

An invariant position would have a variability of one; if 20 amino acids occurred with equal frequency, the variability would be 20 divided by 0.05 equals 400. If, for example, four different amino acids Ser, Asp, Pro, and Thr occurred at a given position, and of 100 sequences available at that position, Ser occurred 80 times, the variability would be 4/0.8 = 5. When any of the amino acid residues sequenced were not identified completely and are listed as Glx (or Asx), two values, separated by a colon, are given in the last three columns. The first value in each of these columns is calculated assuming that only one of the two possibilities, e.g., Glu or Gln (or Asp or Asn) occurred, while the second considers that both were present and maximizes variability. In the variability plots, the horizontal bars indicate the two values.

When two or more amino acids are most common and occur with equal frequency, they are tabulated as a note, and the symbol + is used in the next to last column. If no sequence data have been reported for any position, there are no entries in the last four columns. Variability is not calculated for insertions or if only a single sequence is known. When the translated sequence of a clone corresponds to a previously listed sequence of a plasmacytoma from which it was prepared, only one sequence is listed so that the variability computations are not affected, and a note is included.

If a given sequence is associated with any antibody activity, this is indicated by an asterisk alongside the protein heading, and the antibody specificities are given in a separate list with binding constants if available. The notes list the a-allotypes for the rabbit heavy chain V-region and the b-allotypes for the constant domain of the rabbit kappa light chain. A key reference to the sequence is given; generally the most recent reference since it is usually the most nearly complete, but often several references are included, especially when revisions of a sequence have been made. Notes are now of two types; general notes about a table indicated by the symbol #, and specific notes indicated by the sequence number.

Signal Sequences

The signal (precursor) amino acid sequences of immunoglobulin chains are listed in three tables: one for kappa light chains, one for lambda light chains, and one for heavy chains. They were obtained either by direct sequencing of signal proteins (12-14) or by translating nucleotide sequences from DNA clones. Signal segments range from 17-29 amino acid residues in length and are thus numbered from -29 to -1. Genomic DNA clones contain introns of varying length that interrupt the coding sequence of the precursor within the codon for position -4, and in rare cases for position -6. Thus, the L-gene encodes the leader peptide to position -4 and the 5′ end of the V-gene codes for positions -4 to -1.

The signal amino acid sequences of the T-cell receptors for antigens, β_2-microglobulins, major histocompatibility complex proteins, and complement components are listed in separate tables.

By conformational energy calculations, the core V_κ hydrophobic Leu-Leu-Leu-Trp-Val-Leu-Leu-Leu (MOPC321, MOPC63) exists in an alpha helical conformation, terminated by chain reversal conformations in the four C-terminal residues Trp-Val-Pro-Gly; the four amino terminal residues are compatible with the alpha helix (15).

Variable Region Sequences

The variable regions (16) of immunoglobulins have been shown to contain hypervariable segments in their light (11,17-23) and heavy (22,24-27) chains, of which certain residues have been affinity labeled (28-41). Three hypervariable segments of light chain were delineated from a statistical examination

of sequences of human V_κ, human V_λ, and mouse V_κ light chains aligned for maximum homology (11,22). These and the three corresponding segments of the heavy chains (22,26,27) were hypothesized (11,22) to be the complementarity-determining regions or segments (CDR) containing the residues which make contact with various antigenic determinants, and this has been verified by X-ray diffraction studies at high resolution (42-67). The rest of the V-region constitutes the framework (11,22,66-68). It is convenient to identify the framework segments (FR1, FR2, FR3, and FR4) and the complementarity-determining segments (CDR1, CDR2, and CDR3) with the three CDRs separating the four FRs. The residue numbers for these segments are as follows:

Segment	*Light Chain*	*Heavy Chain*
FR1	1-23 (with an occasional residue at 0, and a deletion at 10 in V_λ chains)	1-30 (with an occasional residue at 0)
CDR1	24-34 (with possible insertions numbered as 27A,B,C,D,E,F)	31-35 (with possible insertions numbered as 35A,B)
FR2	35-49	36-49
CDR2	50-56	50-65 (with possible insertions numbered as 52A,B,C)[a]
FR3	57-88	66-94 (with possible insertions numbered as 82A,B,C)
CDR3	89-97 (with possible insertions numbered as 95A,B,C,D,E,F)	95-102 (with possible insertions numbered as 100A,B,C,D,E,F,G,H,I,J,K)
FR4	98-107 (with a possible insertion numbered as 106A)	103-113

[a] In the rabbit, Mage *et al.* (69) consider position 65 in V_H to be in FR3, since it is allotype related.

In the tables of V-regions, the FR and CDR are separated by horizontal lines for convenience in reading. One mouse kappa light chain, MPC11, has an extra segment of 12 amino acid residues between position 1 and the signal sequence (70). Several chains have internal deletions.

In the tables, the V-genes for the light chains code to amino acid position 95, and the J-minigenes from position 97 to 107 for lambda and 108 for kappa light chains. Position 96 is usually the site of V-J joining by recombination and may be coded partly by the V-gene and partly by the J-minigene. Because the site of V-J recombination could occur at different positions within a codon, different amino acid residues may result at this position. We have changed the location of the inserted residues from 97A-F (2) to 95A-F, since it makes for better alignment by confining chains of different lengths to the V-gene region. In V_κ chains, J1 and J2 were used 5 to 10 times more frequently than J4 and J5 (71).

The V-genes for the heavy chains code up to amino acid position 94 and are followed by the D- and J-minigenes. Because of the extensive variation in the lengths of D-minigenes, the exact boundary between D and J is not always located at the same amino acid position. In addition, the lengths of the J encoded amino acid sequences vary by a few amino acid residues. Moreover, the process of D-J joining appears to involve insertions of extra nucleotides between V and D and between D and J, termed the N region (72-76) and correlates with the appearance of terminal deoxytransferase in B cells (75). The original numbering system for the heavy chains has therefore been retained. Wysocki *et al.* (76) have provided some evidence suggesting a non-random origin for the V_H-D_H junction, perhaps a minigene, rather than random addition of the N nucleotides.

It has become evident that a critical understanding of the architecture of antibody combining sites and the genetics of the generation of diversity and of antibody complementarity will depend to a great extent on the evaluation of a large number of sequences of the variable regions and especially of the complementarity-determining segments of light and heavy chains of immunoglobulins of different species. Ability to locate residues in the site making contact with antigenic determinants (77) and to predict (67,78-82) the structures of antibody combining sites will depend heavily upon such sequences.

Figures 1 and 2 are stereoviews of the α-carbon skeletons of the four Fv regions for which high resolution X-ray structures have been determined, NEWM (44), KOL (62), MCPC603 (47, 48, 63), and J539 (64). The residues in the CDRs are shown as solid circles. In Fig. 1 the combining site is at the

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		INVARIANT RESIDUES	1 ROY	2 AU	3 REI	4 HAU	5 HK101 'CL #	6 SCW	7 AG #	8* WEA	9 HK 137 'CL #	10 HK 134 'CL #	11 DAUDI 'CL	12 WALKER 'CL	13 HF3-16/6	14 HF2-1/13B	15 HF2-18/2	16 HF2-1/17	17 BJ 26 #	18 RFZ	19 PSM	20 HOM	21 ESM IGG	22 ESM IGM	23 WAT
	0		---	---	---	---	#	---	---	---	---	#	---	---	---	---	---	---	---	---	---	---	---	---	---
	1		ASP	ASP	ASP	ASP	ASP	ASP	ASP	ASP	ASP	ASP	ASP	ASP	ASP	ASP	ASP	ASP	ASP	ASP	ASP	ASP	ASP	ASP	ASP
	2		ILE	ILE	ILE	ILE	ILE	ILE	ILE	ILE	ILE	ILE	ILE	ILE	GLN	GLN	GLN	GLN	ILE	ILE	ILE	ILE	GLN	GLN	ILE
	3		GLN	GLN	GLN	GLN	GLN	GLN	GLN	GLN	GLN	GLN	GLN	GLN	GLN	GLN	GLN	GLN	GLN	GLN	GLN	GLN	GLN	GLN	GLN
	4		MET	MET	MET	MET	MET	MET	MET	MET	MET	MET	MET	MET	MET	MET	MET	MET	MET	MET	MET	MET	MET	MET	MET
	5	THR(.98)	THR	THR	THR	THR	THR	THR	THR	THR	THR	THR	THR	THR	THR	THR	THR	THR	THR	THR	THR	THR	THR	THR	THR
	6		GLN	GLN	GLN	GLN	GLN	GLN	GLN	GLN	GLN	GLN	GLN	GLN	GLN	GLN	GLN	GLN	GLN	GLN	GLN	GLN	GLN	GLN	GLN
	7	SER(.95)	SER	SER	SER	SER	SER	SER	SER	SER	SER	SER	SER	SER	SER	SER	SER	SER	SER	SER	SER	SER	SER	SER	SER
	8	PRO(.98)	PRO	PRO	PRO	PRO	PRO	PRO	PRO	PRO	PRO	PRO	PRO	PRO	PRO	PRO	PRO	PRO	PRO	PRO	PRO	PRO	PRO	PRO	PRO
	9		SER	SER	SER	SER	SER	SER	SER	SER	SER	SER	SER	SER	SER	SER	SER	SER	SER	SER	SER	SER	SER	SER	SER
	10		SER	SER	SER	SER	SER	SER	SER	SER	SER	SER	SER	SER	SER	SER	SER	SER	SER	SER	SER	SER	SER	SER	SER
	11		LEU	LEU	LEU	LEU	LEU	LEU	LEU	LEU	LEU	LEU	LEU	LEU	LEU	LEU	LEU	LEU	LEU	LEU	LEU	LEU	LEU	LEU	LEU
	12	SER(.96)	SER	SER	SER	SER	SER	SER	SER	SER	SER	SER	SER	SER	SER	SER	SER	SER	SER	SER	SER	SER	SER	SER	SER
	13		ALA	ALA	ALA	ALA	ALA	ALA	ALA	ALA	ALA	ALA	ALA	ALA	ALA	ALA	ALA	ALA	ALA	ALA	ALA	ALA	ALA	ALA	ALA
	14		SER	SER	SER	SER	SER	SER	SER	SER	SER	SER	SER	SER	SER	SER	SER	SER	SER	SER	SER	SER	SER	SER	SER
	15	VAL(.96)	VAL	VAL	VAL	VAL	VAL	VAL	VAL	VAL	VAL	VAL	VAL	VAL	VAL	VAL	VAL	VAL	VAL	VAL	VAL	VAL	VAL	VAL	VAL
	16	GLY(.99)	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY
	17		ASP	ASP	ASP	ASP	ASP	ASP	ASP	ASP	ASP	ASP	ASP	ASP	ASP	ASP	ASP	ASP	ASP	ASP	ASP	ASP	ASP	ASP	ASP
	18		ARG	ARG	ARG	ARG	ARG	ARG	ARG	ARG	ARG	ARG	ARG	ARG	ARG	ARG	ARG	ARG	ARG	ARG	ARG	ARG	ARG	ARG	ARG
	19	VAL(.97)	VAL	VAL	VAL	VAL	VAL	VAL	VAL	VAL	VAL	VAL	VAL	VAL	VAL	VAL	VAL	VAL	VAL	VAL	VAL	VAL	VAL	VAL	VAL
	20	THR(.96)	THR	THR	THR	THR	THR	THR	THR	THR	THR	THR	THR	THR	THR	THR	THR	THR	THR	THR	THR	THR	THR	THR	THR
	21	ILE(.95)	ILE	ILE	ILE	ILE	ILE	ILE	ILE	ILE	ILE	ILE	ILE	ILE	ILE	ILE	ILE	ILE	ILE	ILE	ILE	ILE	ILE	ILE	ILE
	22		THR	THR	THR	THR	THR	THR	THR	THR	THR	THR	THR	THR	THR	THR	THR	THR	THR	THR	THR	THR	THR	THR	THR
	23	CYS	CYS	CYS	CYS	CYS	CYS	CYS	CYS	CYS	CYS	CYS	CYS	CYS	CYS	CYS	CYS	CYS	CYS	CYS	CYS	CYS	CYS	CYS	CYS
	24		GLN	GLN	GLN	ARG	ARG	GLN	GLN	ARG	ARG	ARG	ARG	ARG	ARG	ARG	ARG	ARG	GLN	GLN	GLN	GLN	ARG	ARG	GLX
	25	ALA(.95)	ALA	ALA	ALA	ALA	ALA	ALA	ALA	ALA	ALA	ALA	ALA	ALA	ALA	ALA	ALA	ALA	ALA	ALA	ALA	ALA	ALA	ALA	ALA
	26		SER	SER	SER	SER	ARG	SER	SER	SER	SER	SER	GLY	SER	SER	SER	SER	SER	SER	ASN	SER	ARG	SER	SER	SER
	27		GLN	GLN	GLN	GLN	GLN	GLN	GLN	GLN	GLN	GLN	HIS	GLN	GLN	GLN	GLN	GLN	GLN	GLN	GLN	HIS	GLX	GLX	GLN
	27A		---	---	---	---	---	---	---	---	---	---	---	---	---	---	---	---	---	---	---	---	---	---	---
	27B		---	---	---	---	---	---	---	---	---	---	---	---	---	---	---	---	---	---	---	---	---	---	---
	27C		---	---	---	---	---	---	---	---	---	---	---	---	---	---	---	---	---	---	---	---	---	---	---
	27D		---	---	---	---	---	---	---	---	---	---	---	---	---	---	---	---	---	---	---	---	---	---	---
	27E		---	---	---	---	---	---	---	---	---	---	---	---	---	---	---	---	---	---	---	---	---	---	---
	27F		---	---	---	---	---	---	---	---	---	---	---	---	---	---	---	---	---	---	---	---	---	---	---
	28		ASP	ASP	ASP	SER	GLY	ASP	ASP	GLY	GLY	GLY	ASN	SER	GLY	GLY	GLY	GLY	SER	VAL	ASP	ASP	SER	SER	ASP
	29		ILE	ILE	ILE	ILE	ILE	ILE	ILE	ILE	ILE	ILE	ILE	ILE	ILE	ILE	ILE	ILE	ILE	ILE	ILE	ILE	ILE	ILE	ILE
	30		SER	SER	ILE	SER	SER	ARG	ASN	ARG	SER	SER	THR	SER	ARG	ARG	ARG	ARG	ASN	SER	ARG	SER	SER	SER	SER
	31		ILE	ASP	LYS	SER	SER	LYS	HIS	ASN	ASN	SER	ASN	ASN	ASN	ASN	ASN	ASN	LYS	LYS	SER	ASN	SER	SER	ASP
	32		PHE	TYR	TYR	TYR	TRP	HIS	TYR	ASP	TYR	TRP	PHE	TYR	ASP	ASP	ASP	ASP	TYR	SER	TYR	TYR	TYR	TYR	TYR
	33		LEU	LEU	LEU	LEU	LEU	LEU	LEU	LEU	LEU	LEU	LEU	LEU	LEU	LEU	LEU	LEU	ALA	LEU	LEU	LEU	LEU	LEU	VAL
	34		ASN	ASN	ASN	SER	ALA	ASN	ASN	THR	ALA	ALA	SER	ASN	GLY	GLY	GLY	GLY	ASN	ASN	ASN	ASN	ASX	ASX	ASN
	35	TRP	TRP	TRP	TRP	TRP	TRP	TRP	TRP	TRP	TRP	TRP	TRP	TRP	TRP	TRP	TRP	TRP	TRP	TRP	TRP	TRP	TRP	TRP	TRP
	36		TYR	TYR	TYR	TYR	TYR	TYR	TYR	TYR	PHE	TYR	TYR	TYR	TYR	TYR	TYR	TYR	TYR	TYR	TYR	PHE	TYR	TYR	
	37		GLN	GLN	GLN	GLN	GLN	ASP	GLN	GLN	GLN	GLN	GLN	GLN	GLN	GLN	GLN	GLN	GLU	GLN	GLN	GLN	GLX	GLX	
	38		GLN	GLN	GLN	GLN	GLN	GLN	GLN	GLN	GLN	GLN	GLN	GLN	GLN	GLN	GLN	GLN	GLN	GLN	GLN	GLN			
	39		LYS	LYS	THR	LYS	LYS	LYS	#	LYS	LYS	LYS	LYS	LYS	LYS	LYS	LYS	LYS	#	ARG	LYS	LYS			
	40	PRO(.95)	PRO	PRO	PRO	PRO	PRO	PRO	PRO	PRO	PRO	PRO	PRO	PRO	PRO	PRO	PRO	PRO	PRO	PRO	GLN	PRO			
	41		GLY	GLY	GLY	GLY	GLU	GLY	#	GLY	GLY	GLU	GLY	GLY					#	GLY	GLY	GLY			
	42		LYS	LYS	LYS	LYS	LYS	LYS	LYS	THR	LYS	LYS	LYS						LYS	GLN	LYS				
	43		ALA	ALA	ALA	ALA	ALA	ALA	ALA	ALA	ALA	ALA	ALA	ALA					ALA	ALA	ALA				
	44	PRO	PRO	PRO	PRO	PRO	PRO	PRO	PRO	PRO	PRO	PRO	PRO	PRO					PRO	PRO	PRO				
	45		LYS	LYS	LYS	GLN	LYS	ARG	LYS	LYS	LYS	LYS	THR	LYS					LYS	LYS	LYS				
	46		LEU	LEU	LEU	VAL	SER	LEU	ILE	ARG	SER	SER	LEU	LEU					LEU	LEU	LEU				
	47	LEU(.98)	LEU	LEU	LEU	LEU	LEU	LEU	LEU	LEU	LEU	LEU	LEU	LEU						LEU	LEU				
	48	ILE(.98)	ILE	ILE	ILE	ILE	ILE	ILE	ILE	ILE	ILE	ILE	ILE	ILE						ILE	ILE				
	49		TYR	TYR	TYR	TYR	TYR	TYR	TYR	TYR	TYR	TYR	TYR	TYR						TYR	TYR				
	50		ASP	ASP	GLU	ALA	ALA	GLY	ASP	GLY	ALA	ALA	ALA	ALA						ASP	ASP				
	51		ALA	ALA	ALA	ALA	ALA	ALA	ALA	ALA	ALA	ALA	VAL	ALA					ASP	ALA	ALA				
	52		SER	SER	SER	SER	SER	SER	SER	THR	SER	SER	SER	SER					SER	ALA	SER				
	53		LYS	ASN	ASN	SER	SER	THR	ASN	SER	SER	SER	ASN	SER					ARG	ASX					
	54	LEU(.98)	LEU	LEU	LEU	LEU	LEU	LEU	LEU	LEU	LEU	LEU	LEU	LEU					LEU	LEU	LEU				
	55		GLU	GLU	GLN	PRO	GLN	GLU	GLU	GLN	GLN	GLN	GLN	GLN					GLU	GLU	GLU				
	56		ALA	SER	ALA	SER	SER	THR	THR	SER	SER	SER	VAL	SER					THR						
	57	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY					GLY	GLY					
	58	VAL(.98)	VAL	VAL	VAL	VAL	VAL	VAL	VAL	VAL	VAL	VAL	VAL	VAL					ASX	VAL					
	59		PRO	PRO	PRO	PRO	PRO	PRO	PRO	PRO	PRO	PRO	PRO	THR					PRO	PRO					
	60	SER	SER	SER	SER	SER	SER	SER	SER	SER	SER	SER	SER	SER					SER						
	61	ARG(.95)	ARG	ARG	ARG	ARG	ARG	ARG	ARG	ARG	ARG	ARG	ARG	ARG					LYS	ARG					
	62	PHE(.95)	PHE	PHE	PHE	PHE	PHE	PHE	PHE	PHE	PHE	PHE	PHE	PHE					VAL	PHE					
	63		SER	SER	SER	SER	SER	SER	SER	SER	SER	SER	SER	SER					SER	THR					
	64	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY					GLY	GLY					
	65		THR	GLY	SER	SER	SER	SER	SER	SER	SER	SER	SER	SER					SER						
	66	GLY(.95)	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY					GLY	GLY					
	67		SER	SER	SER	SER	SER	SER	PHE	SER	SER	SER	SER	SER					SER						
	68		GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY					GLU						
	69		THR	ALA	THR	THR	THR	THR	THR	THR	THR	THR	ALA	THR					THR						
	70		ASP	HIS	ASP	ASP	ASP	ASP	ASP	GLU	ASP	ASP	GLU	ASP					ASP						
	71		PHE	PHE	TYR	PHE	PHE	PHE	PHE	PHE	PHE	PHE	PHE	PHE					VAL						
	72		THR	THR	THR	THR	THR	THR	THR	THR	THR	THR	THR	THR					THR						
	73		PHE	PHE	PHE	LEU	LEU	LEU	PHE	LEU	LEU	LEU	LEU	LEU					VAL						
	74		THR	THR	THR	THR	THR	THR	THR	THR	THR	THR	THR	THR					ASX						
	75	ILE(.95)	ILE	ILE	ILE	ILE	ILE	ILE	ILE	ILE	ILE	ILE	ILE	ILE					GLX						
	76	SER(.95)	SER	SER	SER	SER	SER	SER	SER	ASN	SER	SER	SER	SER					SER						
	77		GLY	SER	SER	SER	SER	THR	GLY	SER	SER	SER	SER	SER					SER						
	78		LEU	LEU	LEU	LEU	LEU	LEU	LEU	LEU	LEU	LEU	LEU	LEU					LEU						
	79		GLN	GLN	GLN	GLN	GLN	GLN	GLN	GLN	GLN	GLN	GLN	GLN					GLN						
	80		PRO	PRO	PRO	PRO	PRO	PRO	PRO	PRO	PRO	PRO	PRO	PRO					PRO						
	81		GLU	GLU	GLU	GLU	GLU	GLU	GLU	GLU	GLU	GLU	GLU	GLU					GLU						
	82		ASP	ASP	ASP	ASP	ASP	ASP	ASP	ASP	ASP	ASP	ASP	ASP					ASP						
	83		ILE	ILE	ILE	PHE	PHE	ILE	ILE	PHE	PHE	PHE	PHE	SER					ILE						
	84	ALA(.98)	ALA	ALA	ALA	ALA	ALA	GLY	ALA	ALA	ALA	ALA	ALA	ALA					ALA						
	85		THR	THR	THR	THR	THR	ASN	THR	THR	THR	THR	THR	THR					PRO						
	86	TYR(.98)	TYR	TYR	TYR	TYR	TYR	TYR	TYR	TYR	TYR	TYR	TYR	TYR					LYS						
	87	TYR(.98)	TYR	TYR	TYR	TYR	TYR	TYR	TYR	TYR	TYR	TYR	TYR	TYR											
	88	CYS	CYS	CYS	CYS	CYS	CYS	CYS	CYS	CYS	CYS	CYS	CYS	CYS											
	89		GLN	GLN	GLN	GLN	GLN	GLN	GLN	LEU	GLN	GLN	GLN	GLN					GLN						
	90		GLN	GLN	GLN	GLN	GLN	GLN	GLN	GLN	GLN	GLN	GLN	GLN					GLN						
	91		PHE	TYR	TYR	ASN	TYR	TYR	TYR	TYR	TYR	TYR	ASN	SER					ARG						
	92		ASP	ASP	GLN	TYR	ASN	ASP	ASP	SER	ASN	ASN	TYR	TYR					ASP						
	93		ASN	TYR	SER	ILE	SER	ASN	THR	SER	SER	SER	ASN	SER					ASP						
	94		LEU	LEU	LEU	THR	TYR	VAL	LEU	PHE	TYR	TYR	PHE	THR					LEU						
	95		PRO	PRO	PRO	PRO	PRO	PRO	PRO	PRO	PRO	PRO	SER	LEU					PRO						
	95A		---	---	---	---	#	---	---	---	---	#	---	---					---						
	95B		---	---	---	---	---	---	---	---	---	---	---	---					---						
	95C		---	---	---	---	---	---	---	---	---	---	---	---					---						
	95D		---	---	---	---	---	---	---	---	---	---	---	---					---						
	95E		---	---	---	---	---	---	---	---	---	---	---	---					---						
	95F		---	---	---	---	---	---	---	---	---	---	---	---					---						
	96		LEU	TRP	TYR	THR	---	ILE	ARG	TRP	---	---	PHE	ILE					TYR						
	97		THR	THR	THR	SER	---	THR	THR	THR	---	---	THR	THR					THR						
	98		PHE	PHE	PHE	PHE	---	PHE	PHE	PHE	---	---	PHE	PHE					LEU						
	99	GLY	GLY	GLY	GLY	GLY	---	GLY	GLY	GLY	---	---	GLY	GLY					GLY						
	100		GLY	GLN	GLN	GLN	---	GLN	GLN	GLN	---	---	GLY	GLN					GLY						
	101	GLY	GLY	GLY	GLY	GLY	---	GLY	GLY	GLY	---	---	GLY	GLY					GLY						
	102	THR(.97)	THR	THR	THR	THR	---	THR	THR	THR	---	---	THR	THR					THR						
	103		LYS	LYS	LYS	ARG	---	ARG	LYS	LYS	---	---	LYS	ARG					LYS						
	104		VAL	VAL	LEU	VAL	---	VAL	LEU	VAL	---	---	VAL	LEU					VAL						
	105		ASP	GLU	GLN	GLU	---	GLU	GLU	GLU	---	---	ASP	GLU					GLU						
	106		PHE	ILE	ILE	ILE	---	ASN	ILE	VAL	---	---	ASN	ILE					MET						
	106A		---	---	---	---	---	---	---	---	---	---	---	---					---						
	107		LYS	LYS	THR	LYS	---	LYS	LYS	LYS	---	---	LYS	LYS					LYS						
	108		ARG	ARG	ARG	ARG	---	GLY	ARG	ARG	---	---	---	---											
	109	THR	THR	THR	THR	THR	---	THR	THR	THR	---	---	---	---											

HUMAN KAPPA LIGHT CHAINS SUBGROUP I (cont'd)

		24 AMYLOID VIII-B	25* LOW	26 DIE	27 CAR A	28 TEI	29 BJ 48	30 CON	31 TRA	32 AMYLOID LEP	33 F-GUI #	34 OU (IOC)	35 DEE	36 GAL (I)	37 JOH	38 KER	39* LAY	40 BRA	41 WES	42 Vb 'CL	43 Vb' 'CL	44 HK102 'CL #	45 EU	46 DEN	47 PAU
	0	---	---	---	---	---	---	---	---	---	---	---	---	---	---	---	---	---	---	---	---	#	---	---	---
	1	ASP	ASP	ASP	ASP	ASP	ASP	ASP	ASP	ASP	ASP	ASP	ASX	ASP	ASP	ASP	ASP	ASP	ASP	ASP	ASP	ASP	ASP	ASP	ASP
	2	ILE	ILE	ILE	ILE	ILE	ILE	ILE	ILE	ILE	ILE	ILE	ILE	ILE	ILE	ILE	ILE	ILE	ILE	ILE	ILE	ILE	ILE	ILE	ILE
	3	GLN	GLN	GLN	GLN	GLN	GLN	GLN	GLN	GLN	GLN	GLN	GLX	GLN	GLN	GLN	GLN	GLN	GLN	GLN	GLN	GLN	GLN	GLN	GLN
	4	MET	MET	MET	MET	MET	MET	MET	MET	MET	MET	MET	MET	MET	MET	MET	MET	MET	MET	MET	MET	MET	MET	MET	MET
	5	THR	THR	THR	THR	THR	THR	THR	THR	THR	THR	THR	THR	THR	THR	THR	THR	THR	THR	THR	THR	THR	THR	THR	THR
	6	GLN	GLN	GLN	GLN	GLN	GLN	GLN	GLN	GLN	GLN	GLX	GLN	GLN	GLN	GLN	GLN	GLX	GLN	GLN	GLN	GLN	GLN	GLN	GLN
	7	SER	SER	SER	SER	SER	SER	SER	SER	SER	SER	SER	SER	SER	SER	SER	SER	SER	SER	SER	SER	SER	SER	SER	SER
	8	PRO	PRO	PRO	PRO	PRO	PRO	PRO	PRO	PRO	PRO	PRO	PRO	PRO	PRO	PRO	PRO	PRO	PRO	PRO	PRO	PRO	PRO	PRO	PRO
	9	SER	SER	SER	SER	SER	SER	SER	SER	SER	SER	SER	SER	SER	SER	SER	SER	SER	SER	SER	SER	SER	SER	SER	SER
FR1	10	SER	SER	SER	SER	SER	SER	SER	SER	SER	SER	SER	SER	SER	SER	SER	SER	SER	SER	SER	SER	thr	thr	thr	thr
	11	LEU	LEU	LEU	LEU	LEU	LEU	LEU	LEU	LEU	LEU	LEU	LEU	LEU	LEU	LEU	LEU	LEU	val	val	val	LEU	LEU	LEU	LEU
	12	SER	SER	SER	SER	SER	SER	SER	SER	SER	SER	SER	SER	SER	SER	SER	SER	SER	SER	SER	SER	SER	SER	SER	SER
	13	ALA	ALA	ALA	ALA	ALA	ALA	ALA	ALA	ALA	ALA	ALA	ALA	ALA	ALA	ALA	val	val	ALA	ALA	ALA	ALA	ALA	ALA	ALA
	14	SER	SER	SER	SER	SER	SER	SER	SER	SER	SER	SER	SER	SER	SER	SER	SER	SER	SER	SER	SER	SER	SER	SER	SER
	15	VAL	VAL	VAL	VAL	VAL	VAL	VAL	VAL	VAL	VAL	VAL	VAL	VAL	VAL	VAL	VAL	VAL	VAL	VAL	VAL	VAL	VAL	VAL	VAL
	16	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY
	17	ASP	ASP	ASP	ASP	ASP	ASP	ASP	ASP	ASP	ASX	ASX	ASP	ASP	ASP	ASP	ASP	glx	ASP	ASP	ASP	ASP	ASP	ASP	ASP
	18	ARG	ARG	ARG	ARG	ARG	ARG	ARG	ARG	ARG	ARG	ARG	ARG	ARG	ARG	ARG	ARG	ARG	ARG	ARG	ARG	ARG	ARG	ARG	ARG
	19	VAL	VAL	VAL	VAL	VAL	VAL	VAL	VAL	VAL	VAL	VAL	VAL	VAL	VAL	ile	VAL	VAL	VAL	VAL	VAL	VAL	VAL	VAL	VAL
	20	THR	THR	THR	THR	THR	THR	THR	THR	THR	THR	THR	THR	THR	THR	THR	THR	THR	THR	THR	THR	THR	THR	THR	THR
	21	ILE	ILE	ILE	ILE	ILE	ILE	ILE	ILE		ILE	ILE	ILE	ILE	ILE	ILE	ILE	ILE	ILE	ILE	ILE	ILE	ILE	ILE	ILE
	22	THR	THR	THR	THR	THR	THR	THR	THR		THR	THR	THR	ile	ser	THR	THR	THR	THR	THR	THR	THR	THR	THR	THR
	23	CYS	CYS	CYS	CYS	CYS	CYS				CYS	CYS	CYS	CYS	CYS	CYS	CYS	CYS	CYS	CYS	CYS	CYS	CYS	CYS	CYS
	24	GLN	ALA									ARG	ARG	ARG		GLN	GLN		ARG	ARG	ARG	ARG	ARG	ARG	ARG
	25	ALA	ALA								ALA	ALA	ALA	ALA		ALA	ALA		ALA	ALA	ALA	ALA	ALA	THR	ALA
	26	SER	SER									SER	GLY	SER		SER	SER		SER	SER	SER	SER	SER	SER	SER
	27	GLN	GLN									GLX	GLN	GLN		GLN	GLN		GLN	GLN	GLN	GLN	GLN	GLN	GLN
	27A	---	---									---	---	---		---	---		---	---	---	---	---	---	---
	27B	---	---									---	---	---		---	---		---	---	---	---	---	---	---
CDR1	27C	---	---									---	---	---		---	---		---	---	---	---	---	---	---
	27D	---	---									---	---	---		---	---		---	---	---	---	---	---	---
	27E	---	---									---	---	---		---	---		---	---	---	---	---	---	---
	27F	---	---									---	---	---		---	---		---	---	---	---	---	---	---
	28	ASX	ASX									THR	SER	GLY		ASP	ASN		ASP	GLY	GLY	SER	SER	SER	SER
	29	ILE	ILE									ILE	VAL	ILE		ILE	VAL		ILE	ILE	ILE	ILE	ILE	ILE	ILE
	30	GLY	SER									SER	ASN	ARG		LYS	ASN		SER	SER	SER	SER	ASN	SER	SER
	31											SER	LYS	ASN			ALA		HIS	SER	SER	SER	THR	ARG	SER
	32	TYR										TYR	TYR	ASP			TYR		TRP	TRP	TRP	TRP	TRP	TRP	SER
	33	LEU										LEU	LEU	LEU			LEU		LEU	LEU	LEU	LEU	LEU	LEU	LEU
	34											ASX	ASN	THR			ASN		ALA	ALA	ALA	ALA	ALA	ALA	ALA
	35	TRP										TRP	TRP	TRP			TRP		TRP	TRP	TRP	TRP	TRP	TRP	TRP
	36											TYR	TYR	TYR			TYR		TYR	TYR	TYR	TYR	TYR	TYR	TYR
	37											GLX	GLN	GLN			GLN		GLN	GLN	GLN	GLN	GLN	GLN	GLX
	38											GLX	GLN	GLN			GLN		GLN	GLN	GLN	GLN	GLN	GLN	GLX
	39											LYS	LYS	LYS			LYS		LYS	LYS	LYS	LYS	LYS	LYS	LYS
	40											PRO	PRO	PRO			PRO		SER	PRO	PRO	PRO	PRO	PRO	PRO
	41											GLY	GLY	GLY			GLY		GLY	GLY	GLY	GLY	GLY	GLY	GLY
FR2	42											LYS	LYS	LYS			LEU		LYS	LYS	LYS	LYS	LYS	GLU	GLX
	43						ALA					ALA	ALA	ALA			ALA		ALA	ALA	ALA	ALA	ALA	ALA	ALA
	44						PRO					PRO	PRO	PRO			PRO		PRO	PRO	PRO	PRO	PRO	PRO	PRO
	45						LYS					ASX	LYS	LYS			LYS		LYS	LYS	LYS	LYS	LYS	LYS	LYS
	46											LEU	VAL	GLU			LEU		LEU	LEU	LEU	LEU	LEU	VAL	LEU
	47											LEU	LEU	LEU			LEU		LEU	LEU	LEU	LEU	LEU	LEU	LEU
	48											ILE		ILE			ILE		ILE	ILE	ILE	ILE	MET	ILE	ILE
	49						GLY					TYR		TYR			TYR		TYR	TYR	TYR	TYR	TYR	TYR	TYR
	50						ASP					ALA	ALA	ALA			GLY		SER	ALA	ALA	ASP	LYS	GLY	GLX
	51						ALA					ALA	ALA	ALA			ALA		ALA	ALA	ALA	ALA	ALA	ALA	
	52						SER					SER	SER	SER			SER		SER	SER	SER	SER	SER	SER	
	53						SER					ASX	SER	ASN			THR		SER	SER	SER	SER	SER	ASN	
CDR2	54						LEU					LEU	LEU	LEU			ARG		LEU	LEU	LEU	LEU	LEU	LEU	
	55						ASX					HIS	LYS	GLN			GLU		GLU	GLN	GLN	GLU	GLU	GLU	
	56						SER					SER	SER	SER			ALA		ASN	SER	SER	SER	SER	SER	
	57						GLY					GLY	GLY	GLY			GLY		GLY	GLY	GLY	GLY	GLY	GLY	
	58						VAL					VAL	VAL	VAL			VAL		VAL	VAL	VAL	VAL	VAL	VAL	
	59						VAL					PRO	PRO	PRO			PRO		PRO	PRO	PRO	PRO	PRO	PRO	
	60						SER					SER	SER	SER			SER		SER	SER	SER	SER	SER	SER	
	61						ARG					ARG	ARG	ARG			ARG		ARG	ARG	ARG	ARG	ARG	ARG	
	62						GLN					PHE	PHE	PHE			PHE		PHE	PHE	PHE	PHE	PHE	PHE	
	63						SER					SER	SER	SER			SER		SER	SER	SER	SER	ILE	SER	
	64						GLY					GLY	GLY	GLY			GLY		GLY	GLY	GLY	GLY	GLY	GLY	
	65						SER					SER	SER	SER			SER		SER	SER	SER	SER	SER	SER	
	66						GLY					GLY	GLY	GLY			GLY		GLY	GLY	GLY	GLY	GLY	GLY	
	67						SER					SER	SER	ALA			SER		SER	SER	SER	SER	SER	SER	
	68						GLY					GLY	GLY	GLY			GLY		GLY	GLY	GLY	GLY	GLY	GLY	
	69						THR					THR	THR	THR			THR		THR	THR	THR	THR	THR	THR	
	70						ASP					ASX	ASP	GLU			ASP		GLU	ASP	ASP	GLU	GLU	GLU	
	71						PRO					PHE	PHE	PHE			PHE		PHE	PHE	PHE	PHE	PHE	PHE	
FR3	72						SER					THR	THR	THR			THR		THR	THR	THR	THR	THR	THR	
	73						LEU					PHE	LEU	LEU			PHE		LEU	LEU	LEU	LEU	LEU	LEU	
	74						ALA					THR	THR	THR			THR		THR	THR	THR	THR	THR	THR	
	75						VAL					ILE	ILE	ILE			ILE		ILE	ILE	ILE	ILE	ILE	ILE	
	76						SER					SER	SER	SER			SER		SER	SER	SER	SER	SER	SER	
	77						ARG					GLY	GLY	SER			SER		SER	SER	SER	SER	SER	SER	
	78											LEU	LEU	LEU			LEU		LEU	LEU	LEU	LEU	LEU	LEU	
	79											GLX	LEU	GLN			GLN		GLN	GLN	GLN	GLN	GLN	GLN	
	80											PRO	PRO	PRO			PRO		PRO	PRO	PRO	PRO	PRO	SER	
	81											GLX	GLU	GLU			GLU		GLU	GLU	GLU	ASP	ASP	ASP	
	82											ASP	ASP	ASP			ASP		ASP	ASP	ASP	ASP	ASP	ASP	
	83											PHE	PHE	PHE			ILE		PHE	PHE	PHE	PHE	PHE	PHE	
	84											ALA	ALA	ALA			ALA		ALA	ALA	ALA	ALA	ALA	ALA	
	85											THR	THR	THR			THR		THR	THR	THR	THR	THR	THR	
	86											TYR	TYR	TYR		TYR	TYR		TYR	TYR	TYR	TYR	TYR	TYR	
	87											TYR	TYR	TYR		TYR	TYR		PHE	TYR	TYR	TYR	TYR	TYR	
	88											CYS	CYS	CYS		CYS	CYS		CYS	CYS	CYS	CYS	CYS	CYS	
	89											GLX	GLX	LEU		GLN	GLN		GLN	GLN	GLN	GLN	GLN	GLN	
	90											GLX	GLX	GLN		GLN	GLN		GLN	GLN	GLN	GLN	GLN	GLN	
	91						GLY					SER	SER	GLN		TYR	TYR		ALA	ALA	ALA	TYR	TYR	TYR	
	92						GLU					TYR	TYR	ASN		ASP	ASN		HIS	ASN	ASN	ASN	ASN	ASP	
	93						SER					SER	THR	SER		ASP	ASN		SER	SER	SER	SER	SER	SER	
	94						ASP					SER	THR	TYR		LEU	TRP		VAL	PHE	PHE	TYR	ASP	PHE	
CDR3	95						SER					PRO	PRO	PRO		PRO	PRO		PRO	PRO	PRO	SER	SER	PRO	
	95A						---					---	---	---		---	---		---	---	---	#	---	---	
	95B						---					---	---	---		---	---		---	---	---	---	---	---	
	95C						---					---	---	---		---	---		---	---	---	---	---	---	
	95D						---					---	---	---		---	---		---	---	---	---	---	---	
	95E						---					---	---	---		---	---		---	---	---	---	---	---	
	95F						---					---	---	---		---	---		---	---	---	---	---	---	
	96						ARG					THR	TYR	ARG		PRO	PRO		LEU	---	---	---	LYS	TYR	
	97						THR					THR	THR	SER		THR	THR		THR	---	---	---	MET	THR	
	98						PHE					PHE	PHE	PHE		PHE	PHE		PHE	---	---	---	PHE	PHE	
	99						GLY					GLY	GLY	GLY		GLY	GLY		GLY	---	---	---	GLY	GLY	
	100						GLN					GLX	PRO	GLN		PRO	GLN		GLY	---	---	---	GLN	GLN	
	101						GLY					GLY	GLY	GLY		GLY	GLY		GLY	---	---	---	GLY	GLY	
FR4	102						THR					THR	THR	THR		THR	THR		THR	---	---	---	THR	THR	
	103						LYS					ARG	LYS	LYS		LYS	LYS		THR	---	---	---	LYS	LYS	
	104						VAL					LEU	VAL	VAL		VAL	VAL		VAL	---	---	---	VAL	LEU	
	105						GLU					GLX	GLU	GLU		ASP	GLU		ASP	---	---	---	GLU	GLU	
	106						VAL					ILE	MET	ILE		LEU	VAL		ILE	---	---	---	VAL	ILE	
	106A						---					---	---	---		---	---		---	---	---	---	---	---	
	107						LYS					LYS	THR	LYS		LYS	LYS		LYS	---	---	---	LYS	LYS	
	108											ARG	ARG	ARG			ARG		ARG	---	---	---	GLY	ARG	
	109											THR	THR	THR								---	THR	THR	

HUMAN KAPPA LIGHT CHAINS SUBGROUP I (cont'd)

		48 HBJ 4	49 FRA	50 GR*	51 PAUL	52 MON	53* HEI	54 POT	55 S-GUI #	56 AMYLOID BAN #	57 BJ 19 #	58 BEL	59 JBL #	60 PAP	61 CAR	62 MEV	63 BI	64 AMYLOID ES305 #	65 CRA	66* DAV	67* FIN	68 KA	69 Vd *CL	70 LUX	71 NE	72 Va* CL
	0	---	---	---	---	---	---	---	---	---	---	---	---	---	---	---	---	---	---	---	---	---	---	---	---	---
	1	ASP	ASP	ASP	ASP	ASP	ASP	ASP	ASP	ASP	ASP	ASP	ASP	ASP	ASP	ASP	ASP	ASP	ASP	ASP	ASP	ASP	ASP	ASP	ASP	ala
	2	ILE	ILE	ILE	ILE	ILE	ILE	ILE	ILE	ILE	ILE	ILE	ILE	ILE	ILE	val	ILE	ILE	ILE	ILE	ILE	ILE	ILE	ILE	ILE	ILE
	3	GLN	GLN	GLN	GLN	GLN	GLN	GLN	GLN	GLN	GLN	GLN	GLN	GLN	GLN	GLN	GLN	GLN	GLN	GLN	GLN	GLN	GLN	GLN	his	GLN
	4	MET	MET	MET	MET	MET	MET	MET	MET	leu	leu	leu	MET	MET	MET	MET	MET	leu	MET	MET	MET	leu	leu	leu	leu	leu
	5	THR	THR	THR	THR	THR	THR	THR	THR	THR	THR	THR	THR	THR	THR	THR	THR	THR	THR	THR	THR	THR	THR	THR	THR	THR
	6	GLN	GLN	GLN	GLN	GLN	GLN	GLN	GLN	GLN	GLN	GLN	GLN	GLN	GLN	GLN	GLN	GLN	GLN	GLN	GLN	GLN	GLN	GLN	GLN	GLX	GLN
	7	SER	SER	SER	SER	SER	SER	SER	ala	SER	SER	SER	SER	SER	SER	SER	SER	SER	SER	SER	SER	SER	SER	SER	SER	SER	SER
	8	PRO	PRO	PRO	PRO	PRO	PRO	PRO	PRO	PRO	PRO	PRO	PRO	PRO	PRO	PRO	PRO	PRO	PRO	PRO	PRO	PRO	PRO	PRO	PRO	PRO	PRO
	9	SER	SER	SER	SER	SER	SER	ala	SER	SER	SER	SER	SER	SER	SER	SER	SER	SER	SER	SER	SER	SER	SER	SER	SER	SER	SER
FR 1	10	thr	thr	thr	thr	thr	thr	SER	SER	SER	SER	SER	SER	SER	thr	SER	pro	SER	SER	SER	thr	pro	phe	phe	SER	SER	SER
	11	LEU	LEU	LEU	LEU	LEU	LEU	LEU	LEU	LEU	LEU	LEU	LEU	LEU	LEU	LEU	LEU	LEU	LEU	LEU	LEU	LEU	LEU	LEU	LEU	LEU	LEU
	12	SER	SER	SER	SER	SER	SER	SER	SER	SER	SER	SER	SER	SER	SER	SER	SER	SER	SER	SER	SER	SER	SER	SER	SER	SER	SER
	13	ALA	ALA	ALA	ALA	ALA	ALA	ALA	ALA	ALA	ALA	ALA	ALA	val	ALA	ALA	ALA	ALA	ALA	thr	thr	val	ALA	ALA	ALA	ALA	ALA
	14	SER	SER	SER	SER	SER	SER	SER	SER	SER	SER	SER	tyr	SER	SER	SER	SER	SER	SER	val	val	SER	SER	SER	SER	SER	SER
	15	VAL	VAL	VAL	VAL	VAL	VAL	VAL	VAL	VAL	VAL	VAL	VAL	VAL	VAL	VAL	VAL	VAL	leu	VAL	VAL	VAL	VAL	VAL	VAL	VAL	VAL
	16	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	arg	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY
	17	ASP	ASP	ASP	ASP	ASP	ASP	ASP	ASX	ASP	ASP	ASP	ASP	ASP	ASP	ASP	ASP	ASP	ASP	ASP	ASP	ASP	ASP	ASP	ASP	ASX	ASP
	18	ARG	ARG	ARG	ARG	ARG	ARG	ARG	ARG	ARG	ARG	ARG	ARG	ARG	ARG	ARG	ser		ARG	ARG	ARG	ARG	ARG	ARG	ARG	ARG	ARG
	19	VAL	VAL	VAL	VAL	VAL	VAL	VAL	VAL	VAL	VAL	VAL	VAL	VAL	VAL	VAL	VAL	VAL	VAL	VAL	VAL	VAL	VAL	VAL	VAL	VAL	VAL
	20	THR	THR	THR	THR	THR		THR	THR	THR	THR	THR	THR	THR	ala	ile	THR	#	THR	THR	THR	THR	THR	THR	THR	THR	THR
	21	ILE	ILE	ILE	ILE	ILE		ILE	ILE	ILE	ILE	ILE	ILE	ILE	ILE	ILE	ILE	THR	ILE	ILE	THR	ILE	ILE	ILE	ILE	ILE	ILE
	22	THR	THR	THR	THR	THR		THR	THR	THR	THR	THR	ala	ala	THR	THR	THR	THR	THR	THR	THR	THR	THR	THR	THR	THR	THR
	23	CYS	CYS	CYS	CYS			CYS	CYS	CYS	CYS	CYS	CYS		CYS	CYS	CYS	CYS		CYS	CYS	CYS	CYS			CYS	CYS
	24	ARG	ARG	ARG	ARG				ARG	ARG	GLN	GLX	ARG		ARG	ARG	GLN	GLN		ASP	ASP	GLU	ARG		GLX	ARG
	25	ALA	ALA	ALA	ALA				ALA	ALA	ALA	ALA	ALA		ALA	ALA	ALA	ALA		ALA	ALA	ALA	ALA		ALA	ALA
	26	SER	SER	SER	SER					SER	SER	SER	SER		SER	SER	SER	SER		SER	SER	SER	SER		SER	SER
	27	GLN	GLX	ARG	GLN					GLN	GLN	GLX	GLN		GLN	GLN	GLN	GLU		GLN	GLN	GLN	GLN		GLX	GLN
	27A	---	---	---	---					---	---	---	---		---	---	---	---		---	---	---	---		---	---
	27B	---	---	---	---					---	---	---	---		---	---	---	---		---	---	---	---		---	---
CDR 1	27C	---	---	---	---					---	---	---	---		---	---	---	---		---	---	---	---		---	---
	27D	---	---	---	---					---	---	---	---		---	---	---	---		---	---	---	---		---	---
	27E	---	---	---	---					---	---	---	---		---	---	---	---		---	---	---	---		---	---
	27F	---	---	---	---					---	---	---	---		---	---	---	---		---	---	---	---		---	---
	28	SER	ASX	SER	SER					SER	ASP	ASX	SER		ASN	SER	ASP	ALA		ASX	ASX	THR	GLY		ASX	GLY
	29	VAL	ILE	ILE	ILE					VAL	ILE	ILE	ILE		ILE	SER	ILE	#		ILE	ILE	VAL	ILE		ILE	ILE
	30	ASN	ASX	SER	SER					TYR	ASN	SER	SER		SER	VAL	ARG			ASX	ASX	LEU	SER		SER	SER
	31	ASN	ASX	SER	SER					ASN	THR	LYS	THR		SER	ASP	ASN	ASN		SER	SER	SER	SER		ASX	SER
	32	TRP	TYR	TRP	SER					TYR	PHE		PHE		TRP	TYR	SER	TYR		TRP	TRP	TYR	TYR		TYR	ALA
	33	LEU	LEU	LEU						VAL	LEU		LEU		LEU	LEU	LEU	LEU		LEU	LEU	LEU	LEU		LEU	LEU
	34	ALA	ALA	ALA						ALA	ASN		#		ALA	ASN	ILE			ILE	ILE	ASN	ALA		ASX	ALA
	35	TRP	TRP	TRP						TRP	TRP		TRP		TRP	TRP	TRP	TRP		TRP	TRP	TRP	TRP		TRP	TRP
	36	TYR	TYR	TYR						PHE	TYR		TYR		TYR	TYR	TYR	TYR		TYR	TYR	TYR	TYR		TYR	TYR
	37	GLN	GLX	GLN						GLN	GLU		GLN		GLN	GLN	GLN			GLN	GLN	GLN	GLN		GLX	GLN
	38	GLU	GLX	GLY						GLN	GLN		GLN		GLN	GLN	GLN			GLN	GLN	GLN	GLN		GLX	GLN
	39	LYS	LYS	ARG						LYS	#		LYS		LYS	LYS	LYS			TYR	TYR	LYS	LYS		LYS	LYS
	40	PRO	PRO	PRO						PRO	PRO		PRO		PRO	PRO	PRO			PRO	PRO	PRO	PRO		PRO	PRO
FR 2	41	GLY								GLY	#	GLY	GLY		GLY	GLY	GLY					GLY	GLY		GLY	GLY
	42	GLX								LYS	LYS	LYS	LYS		LYS	LYS	LYS					LYS	LYS		GLX	LYS
	43	ALA								ALA	ALA	PRO	ALA		ALA	ALA	ALA					ALA	ALA		ALA	ALA
	44	PRO								PRO	PRO	PRO	PRO		PRO	PRO	PRO					PRO	PRO		PRO	PRO
	45	LYS								LYS	LYS	GLU	LYS		LYS	LYS	LYS					LYS	LYS		LYS	LYS
	46	LEU								SER	LEU	LEU	LEU		VAL	LEU	PHE					LEU	LEU		VAL	LEU
	47	LEU								LEU	LEU	LEU	LEU		LEU	LEU	LEU					LEU	LEU		MET	LEU
	48	ILE								ILE	ILE	ILE			ILE	ILE	ILE					ILE	ILE		ILE	ILE
	49	SER								TYR	TYR	TYR	TYR		TYR	PHE	TYR					TYR	TYR		TYR	TYR
	50	LYS								ASP	ASP	ASP			LYS	ASP	ASP					ALA	ALA			ASP
	51	THR								ALA	ALA	ALA			SER	THR	ALA					ALA	ALA			ALA
CDR 2	52	SER								SER	SER	SER			SER	SER	GLU					SER	SER			SER
	53	SER								THR	SER	THR			SER	ASN	ASN					SER	THR			SER
	54	LEU								LEU	LEU	LEU			LEU	LEU	LEU					LEU	LEU			LEU
	55	GLU								GLN	GLU	LYS			GLU	GLN	GLU					GLU	GLN			GLU
	56	ARG								SER	THR	THR			SER	SER	ILE					THR	SER			SER
	57	GLY								GLY	GLY	GLY			GLY	GLY	GLY					GLY	GLY			GLY
	58	VAL								VAL	VAL	VAL			VAL	VAL	VAL					VAL	VAL			VAL
	59	PRO								PRO	GLX	PRO			PRO	PRO						PRO	PRO			PRO
	60	SER								SER	SER	SER			SER	SER	SER					SER	SER			SER
	61	ARG								ASN	ARG	ARG			ARG	ARG	ARG					ARG	ARG			ARG
	62	PHE								PHE	PHE	PHE			PHE	PHE	PHE					PHE	PHE			PHE
	63	ALA								THR	LEU	SER			SER	SER	ARG					SER	SER			SER
	64	GLY								GLY	GLY	GLY			GLY	GLY	GLY					GLY	GLY			GLY
	65	SER								SER	SER	SER			SER	GLY	SER					GLN	SER			SER
	66	GLY								GLY	ASX	GLY			GLY	ARG	GLY					GLY	GLY			GLY
	67									SER	PHE	SER			SER	SER	SER					SER	SER			SER
	68									GLY	ASX	GLU			GLY	GLY	GLY					GLY	GLY			GLY
	69									THR	THR	THR			THR	THR	THR					THR	THR			THR
	70									ASP	LYS	HIS			ASP	ASP	ASP					ASX	GLU			ASP
FR 3	71									PHE		PHE			PHE	PHE	PHE					PHE	PHE			PHE
	72									ILE		THR			THR	THR	ALA					THR	THR			THR
	73									LEU		LEU			LEU	LEU	LEU					PHE	LEU			LEU
	74									THR		THR			THR	THR	SER					THR	THR			THR
	75									ILE		ILE			ILE	ILE	ILE					ILE	ILE			ILE
	76									SER					SER	SER	SER					SER	SER			SER
	77									SER		SER			SER	SER	SER					SER	SER			SER
	78									LEU		LEU			LEU	LEU	LEU					VAL	LEU			LEU
	79									GLN		GLN			GLX	GLN	GLN					GLX	GLN			GLN
	80									PRO		PRO			PRO	PRO	PRO					PRO	PRO			PRO
	81									GLU		ALA			ASX	ASP	GLU					GLX	GLU			GLU
	82									ASP		ASP			ASX	ASP	ASP					ASX	ASP			ASP
	83									PHE		PHE			PHE	PHE	PHE					PHE	PHE			PHE
	84									ALA		ALA			ALA	ALA	ALA					ALA	ALA			ALA
	85									THR		THR			THR	THR	THR					THR	THR			THR
	86									TYR		TYR			TYR	TYR	TYR					TYR	TYR			TYR
	87									TYR		TYR			TYR	TYR	TYR					TYR	TYR			TYR
	88									CYS		CYS			CYS	CYS	CYS					CYS	CYS			CYS
	89									GLN		GLN			GLN	GLN	GLN					GLN	GLN			GLN
	90									GLN		GLN			GLN	GLN	GLN					GLX	GLN			GLN
	91									TYR	PHE	TYR			TYR	SER	TYR					TYR	LEU			PHE
	92									ASN	ASP	ASX			ASN	TYR	TYR					LEU	ASN			ASN
	93									SER	ASP	HIS			THR	THR	ASN					ASP	SER			SER
	94									TYR	LEU	PHE			PHE	ASN	LEU					LEU	TYR			TYR
	95									PRO	PRO	PRO			---	PRO	PRO					PRO	PRO			PRO
CDR 3	95A									---	---	---			---	GLU	---					---	---			---
	95B									---	---	---			---	---	---					---	---			---
	95C									---	---	---			---	---	---					---	---			---
	95D									---	---	---			---	---	---					---	---			---
	95E									---	---	---			---	---	---					---	---			---
	95F									---	---	---			---	---	---					---	---			---
	96									TYR	TYR	LEU			PHE	VAL	TYR					ARG	---			---
	97									THR	THR	THR			THR	THR	THR					THR	---			---
	98									PHE	PHE	PHE			PHE	PHE	PHE					PHE	---			---
	99									GLY	GLY	GLY			GLY	GLY	GLY					GLY	---			---
	100									GLN	PRO	GLY			PRO	GLY	GLN					GLN	---			---
	101									GLY	GLY	GLY			GLY	GLY	GLY					GLY	---			---
FR 4	102									THR	THR	THR			THR	THR	THR					THR	---			---
	103									LYS	LYS	GLU			LYS	THR	LYS					LYS	---			---
	104									#	VAL	VAL			VAL	VAL	LEU					VAL	---			---
	105									#	GLU	GLU			ASP	ASP	GLU					ASP	---			---
	106									ILE	LEU	VAL			ILE	ILE	ILE					LEU	---			---
	106A									---	---	---			---	---	---					---	---			---
	107									LYS	LYS	LYS			LYS	LYS	LYS					LYS	---			---
	108									ARG					ARG	ARG	ARG					ARG	---			---
	109														THR		THR					THR	---			---

HUMAN KAPPA LIGHT CHAINS SUBGROUP I (cont'd)

		73 NI	74 PW #	75 AMYLOID X	76 ALE	77 SHE	78 ADA	79 KUE	80 GO	81 BOL	82 RI #	83 Ve 'CL	84 OCO	85 V13 'CL	86 V18A 'CL	87 V19A 'CL	88 V19B 'CL	89 V18B 'CL	90 HF6-21/28	91 SAC	92* WAG	93 HBJ 1	94 AMYLOID 547	95 WEB	96 HOE
	0	---	---	---	---	---	---	---	---	---	pca	---	---	---	---	---	---	---	---	---	---	---	---	---	---
	1	ASP	ASP	ASP	ASX	ASP	ASP	ASP	ASP	ASP	ASP	ala	ASX	val	ASP	ala	ala	ala	ASP	ASP	ASP	ASP	ASP	ASP	ASP
	2	ILE	ILE	ILE	ILE	ILE	ILE	ILE	val	ILE	ILE	ILE	ILE	ILE	pro	gln	ILE	gln	val	ILE	ILE	ILE	ILE	ILE	ILE
	3	GLN	his	GLN	GLX	GLN	GLN	GLN	GLN	GLN	GLN	arg	GLX	trp	val	val	asp	val	val	GLN	GLN	leu	GLX	GLN	GLN
	4	MET	MET	MET	MET	leu	val	MET	MET	ile	MET	MET	MET	MET	MET	leu	MET	leu	MET	MET	MET	MET	MET	MET	MET
	5	THR	THR	THR	THR	THR	THR	THR	THR	met	THR	THR	THR	THR	THR	THR	THR	THR	THR	THR	THR	THR	THR	THR	THR
	6	GLN	GLN	GLN	GLX	GLN	GLN	GLN	GLX	GLX	GLN	GLN	GLX	GLN	GLN	GLN	GLN	GLN	GLN	GLN	GLN	GLN	GLN	GLN	GLN
	7	SER	SER	SER	SER	SER	SER	SER	SER	SER	SER	SER	SER	SER	thr	thr	thr	thr	SER	SER	SER	SER	SER	SER	SER
	8	PRO	PRO	ala	PRO	PRO	PRO	PRO	PRO	PRO	PRO	PRO	PRO	PRO	PRO	PRO	PRO	glu	PRO	PRO	PRO	PRO	PRO	PRO	PRO
	9	SER	SER	SER	SER	thr	SER	SER	SER	SER	SER	SER	SER	SER	SER	ala	ala	SER	leu	SER	SER	thr	SER	SER	SER
FR1	10	SER	SER	SER		SER	SER	thr	phe	SER	thr	SER	SER	leu	SER	SER	SER	pro	SER	SER	SER	SER	SER	SER	thr
	11	LEU	LEU	LEU		LEU	LEU	gln	val	val	LEU	phe	LEU	LEU	thr	val	val	val	LEU	LEU	LEU	LEU	LEU	val	LEU
	12	SER	SER	SER	SER	SER	SER	pro	SER	SER	SER	SER	val	SER	SER	SER	glu	SER	pro	SER	SER	SER	SER	SER	SER
	13	ALA	ALA	ALA	ALA	ALA	val	ALA	ALA	ALA	ALA	ALA	ser	ALA	ALA	ALA	ALA	ALA	val	ALA	ALA	ALA	ALA	ALA	ALA
	14	thr	SER	SER	SER	SER	phe	SER	SER	SER	SER	pro	SER	SER	ala	ala	ala	pro	thr	SER	SER	SER	SER	SER	SER
	15	VAL	VAL	VAL	VAL	VAL	VAL	VAL	VAL	VAL	VAL	thr	VAL	thr	VAL	VAL	VAL	VAL	leu	VAL	VAL	VAL	VAL	VAL	VAL
	16	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY			
	17	ASP	ASP	ASP	ASP	ASX	ASP	ASP	ASX	ASX	ASP	ASP	ASX	ASP	gly	gly	gly	gly	gly	ASP	ASP	ASP			
	18	ARG	ARG	ARG	ARG	ARG	ARG	ARG	ARG	ARG	gly	ARG	leu	ARG	thr	thr	thr	thr	pro	---					
	19	VAL	VAL	VAL	VAL	VAL	VAL	VAL	VAL	VAL	VAL	VAL	VAL	VAL	VAL	VAL	ile	VAL	ala	---					
	20	THR	THR	ile	THR	THR	THR	THR	THR	THR	THR	THR	THR	THR	THR	THR	THR	THR	ser	---					
	21	leu	val	ILE	leu	phe	ILE	ILE	ILE	ILE	ILE	ILE	ILE	ILE	ILE	ILE	ILE	ILE	ILE	---					
	22	leu	arg		THR	THR	THR	THR	THR	THR	ser	THR	THR	ser	asn	ASN	asn	asn	ser	---					
	23	CYS	CYS	CYS	CYS	CYS	CYS	CYS	CYS	CYS	CYS	CYS	CYS	CYS	CYS	CYS	CYS	CYS	CYS	---					
	24	GLU	ARG	GLX	ARG	GLX	GLX	ARG	ARG	ARG	ARG	ARG	GLX	ARG	GLN	GLN	GLN	GLN	ARG	---					
	25	ALA	ALA	ALA		ALA	ALA	ALA	ALA	ALA	ALA	ALA	ALA	MET	SER	ALA	ALA	ALA	SER	---					
	26	SER	SER			SER	SER	SER	SER	SER	SER	SER	SER	SER	SER	SER	SER	SER	SER	---					
	27	GLN	GLX	GLX		GLX	GLX	GLN		GLX	GLX	GLN	GLX	GLN	GLN	GLU	GLU	GLN	GLN	---					
	27A	SER	---	---		---	---	---		---	---	---	---	---	ASN	---	---	SER	SER	---					
	27B	VAL	---	---		---	---	---		---	---	---	---	---	VAL	---	---	VAL	LEU	---					
CDR1	27C	LEU	---	---		---	---	---		---	---	---	---	---	---	---	---	---	VAL	---					
	27D	GLU	---	---		---	---	---		---	---	---	---	---	---	---	---	---	TRP	---					
	27E	---	---	---		---	---	---		---	---	---	---	---	---	---	---	---	SER	---					
	27F	---	---	---		---	---	---		---	---	---	---	---	---	---	---	---	---	---					
	28	SER	SER	ASX		ASX	ASX	SER		GLY	SER	GLY	ASX	GLY	TYR	SER	SER	TYR	ASP	---					
	29	GLY	ILE	ILE		ILE	ILE	ILE		ILE	ILE	ILE	ILE	ILE	SER	ILE	ILE	ASP	GLY	---					
	30	ASN	GLY			SER		ASN			SER	SER	SER	SER	ASN	SER	SER	ASN	ARG	---					
	31	THR		PRO		ASX	ASX	ILE				SER	ASX	SER	ASN	SER	SER	ASN	SER	---					
	32	PHE	TYR	TYR		TYR	TYR	TRP				TYR	TYR	SER	TYR	TYR	TRP	TRP	TYR	---					
	33	LEU	SER	LEU		LEU	LEU	LEU				LEU		LEU	LEU	LEU	LEU	LEU	LEU	---					
	34	ALA	ASX			ASX	ASX	ALA				ALA		ALA	SER	ASN	ALA	SER	GLU	---					
	35	TRP	TRP			TRP	TRP	TRP				TRP		TRP	TRP	TRP	TRP	TRP	TRP	---					
	36	TYR		TYR		TYR	TYR	TYR				TYR		TYR	PHE	TYR	TYR	TYR	TYR	---					
	37	GLN	GLN			HIS	GLX	GLN				GLN		GLN	GLN	GLN	GLN	GLN	GLN	---					
	38	GLN	GLN			GLX	TYR	GLN				GLN		GLN	GLN	GLN	GLN	GLN	GLN	---					
	39	LYS	LYS			LYS	LYS	LYS				LYS		LYS	LYS	LYS	LYS	LYS	LYS	---					
	40	PRO				PRO	PRO	PRO				PRO		PRO	PRO	LEU	PRO	PRO	PRO	---					
	41	LYS						GLU				GLY		GLY	GLY	GLY	GLY	GLY		---					
FR2	42	LYS						LYS				LYS		LYS	GLN	GLN	GLN	GLN		---					
	43	ALA						ALA				ALA		ALA	PRO	PRO	PRO	PRO		---					
	44	PRO						PRO				PRO		PRO	PRO	PRO	PRO	PRO		---					
	45	LYS						LYS				LYS		GLU	LYS	LYS	LYS	LYS		---					
	46	LEU						LEU				LEU		LEU	LEU	LEU	LEU	LEU		---					
	47	LEU						LEU				LEU		LEU	LEU	LEU	LEU	LEU		---					
	48	ILE						ILE				ILE		ILE	ILE	ILE	ILE	ILE		---					
	49	TYR						TYR				TYR		TYR	TYR	TYR	TYR	TYR		---					
	50	ASP						LYS				ALA		ALA	GLY	TYR	GLU	ASP		LYS					
	51	ALA						ALA				ALA		ALA	ALA	ALA	ALA	ALA		SER					
CDR2	52	SER						SER				SER		SER	SER	SER	SER	SER		---					
	53	ASN						THR				THR		THR	LYS	THR	LYS	LYS		---					
	54	LEU						LEU				LEU		LEU	LEU	LEU	LEU	LEU		---					
	55	GLU						GLU				GLN		GLN	ALA	ALA	ALA	ALA		---					
	56	THR						THR				SER		SER	SER	SER	SER	SER		---					
	57	GLY						GLY				GLY		GLY	GLY	GLY	GLY	GLY		---					
	58	VAL						VAL				VAL		VAL	VAL	VAL	VAL	VAL		---					
	59	PRO						PRO				PRO		PRO	PRO	PRO	PRO	PRO		---					
	60	SER						SER				SER		SER	SER	SER	SER	SER		---					
	61	ARG						ARG				ARG		ARG	ARG	ARG	ARG	ARG		---					
	62	PHE						PHE				PHE		PHE	PHE	PHE	PHE	PHE		---					
	63	SER						SER				SER		SER	SER	LYS	SER	SER		---					
	64	GLY						GLY				GLY		GLY	GLY	GLY	GLY	GLY		---					
	65	SER						SER				SER		SER	SER	SER	SER	SER		---					
	66	GLY						GLY				GLY		GLY	GLY	GLY	GLY	GLY		---					
	67	SER						SER				SER		SER	SER	SER	SER	SER		---					
	68	GLY						GLY				GLY		GLY	GLY	GLY	GLY	GLY		---					
	69	THR						THR				THR		THR	LYS	THR	THR	THR		---					
	70	ASP						GLN				ASP		ASP	GLN	GLU	GLN	GLN		---					
	71	PHE						PHE				PHE		PHE	PHE	TYR	PHE	PHE		---					
FR3	72	THR						THR				THR		THR	THR	THR	THR	THR		---					
	73	PHE						LEU				LEU		LEU	LEU	LEU	LEU	LEU		---					
	74	THR						THR				THR		THR	THR	THR	THR	THR		---					
	75	ILE						ILE				ILE		ILE	ILE	ILE	ILE	ILE		---					
	76	SER						ASN				SER		SER	SER	SER	SER	SER		---					
	77	GLY						SER				CYS		CYS	GLY	GLY	GLY	GLY		---					
	78	LEU						LEU				LEU		LEU	VAL	VAL	VAL	VAL		---					
	79	GLX						GLN				GLN		GLN	GLN	GLN	GLN	GLN		---					
	80	PRO						PRO				SER		SER	CYS	CYS	CYS	CYS		---					
	81	GLX						ASP				GLU		GLU	ASP	ASP	ASP	ASP		---					
	82	ASX						ASP				ASP		ASP	ASP	ASP	ASP	ASP		---					
	83	PHE						PHE				PHE		PHE	ALA	ALA	ALA	ALA		---					
	84	ALA						ALA				ALA		ALA	ALA	ALA	ALA	ALA		---					
	85	VAL						THR				THR		THR	THR	THR	THR	THR		---					
	86	TYR						TYR				TYR		TYR	TYR	TYR	TYR	TYR		---					
	87	TYR						TYR				TYR		TYR	TYR	TYR	TYR	TYR		---					
	88	CYS						CYS				CYS		CYS	CYS	CYS	CYS	CYS		CYS					
	89	GLN						GLN				GLN		GLN	ALA	GLN	GLN	GLN		GLX					
	90	GLX						GLN				GLN		GLN	GLY	HIS	GLY	GLY		GLX					
	91	TYR						TYR				TYR		TYR	TYR	GLY	GLY	SER		GLX					
	92	ASP						SER				TYR		TYR	TYR	TYR	TYR	TYR		ASX					
	93	THR						ARG				SER		SER	TYR	ILE	TYR	TYR		ALA					
	94	LEU						TYR				TYR		PHE	SER	TYR	ASN	SER		ALA					
CDR3	95	PRO						PRO				PRO		PRO	GLY	SER	SER	SER		THR					
	95A	---						---				---		---	SER	SER	GLY	GLY		---					
	95B	---						---				---		---	GLY	GLY	TRP	TRP		---					
	95C	---						---				---		---	THR	ASP	TYR	TYR		---					
	95D	---						---				---		---	ASP					---					
	95E	---						---				---		---						---					
	95F	---						---				---		---						---					
	96	SER						TYR				---		---						ILE					
	97	THR						THR				---		---						PRO					
	98	PHE						PHE				---		---						ILE					
	99	GLY						GLY				---		---						GLY					
	100	VAL						GLN				---		---						GLY					
	101	GLY						GLY				---		---						GLY					
	102	SER						THR				---		---						THR					
FR4	103	LYS						LYS				---		---						LYS					
	104	VAL						LEU				---		---						VAL					
	105	GLU						ASP				---		---						ASX					
	106	SER						ILE				---		---						VAL					
	106A	---						---				---		---						---					
	107	LYS						LYS				---		---						LYS					
	108	ARG						ARG				---		---						ARG					
	109	THR						THR				---		---						THR					

HUMAN KAPPA LIGHT CHAINS SUBGROUP I (cont'd)

		97 LOD	98 HBJ 10	99 BEN	100 GR	101 MAA	102 MUK	103 AMYLOID 594	104* MAR	105 AMYLOID	106 BJ	107 HBJ 6	108 PEN	109 AMYLOID MS #	110 CL*	111 GM131 CL #	# OF SEQUENCES	# OF AMINO ACIDS	OCCURRENCES OF MOST COMMON AMINO ACID
	0	---	---	---	---	---	---	---	---	---	---	---	---	---	---		1	1	1(PCA)
	1	ASP	ASP	ASP	ASP	ASP	ASP	ASP	ASP	ASP	ASX	ASP	ASP	ASP	---		109	3 : 4	103(ASP) : 99(ASP)
	2	ILE	ILE	ILE	ILE	ILE	ILE	ILE	ILE	ILE		ILE	ILE	#	---		107	4	101(ILE)
	3	GLN	GLN	GLN	GLN	GLN	GLN	GLN	GLN	glu		GLN	GLN	GLN	---		108	8	97(GLN) : 93(GLN)
	4		MET	MET	MET	leu	MET	MET	leu	MET	MET	MET	MET	MET	---		108	4	93(MET)
	5	THR	THR	THR	THR	THR	THR	THR	THR	pro	THR	THR		THR	---		108	3	106(THR)
	6	GLN	GLN	GLN	GLN	GLN	GLN	GLN	GLN	GLN	GLN	GLN			---		107	1 : 2	107(GLN) : 100(GLN)
	7	SER	SER	SER	SER	SER	SER	SER	PRO	SER					---		105	3	100(SER)
	8	PRO	PRO	PRO	PRO	PRO	PRO	PRO	PRO	PRO					---		105	3	103(PRO)
	9	SER	SER	SER	SER	SER	SER	SER	SER	SER					---		105	4	99(SER)
FR1	10	thr	SER	SER	SER	thr	SER	SER	SER	SER					---		104	5	81(SER)
FR1	11		LEU	LEU	LEU	LEU	LEU	LEU	LEU	LEU					---		103	5	91(LEU)
FR1	12	SER	SER	SER	SER	SER	SER								---		102	4	98(SER)
FR1	13	ALA	ALA	ALA	val	ALA									---		101	4	91(ALA)
FR1	14	-	SER												---		97	7	86(SER)
FR1	15	VAL													---		97	3	93(VAL)
FR1	16														---		93	2	92(GLY)
FR1	17														---		93	3 : 4	87(ASP) : 79(ASP)
FR1	18	-									ARG				---		90	6	82(ARG)
FR1	19										VAL				---		91	3	88(VAL)
FR1	20										THR				---		91	4	87(THR)
FR1	21										ILE				---		88	4	84(ILE)
FR1	22										THR				---		88	7	75(THR)
FR1	23										CYS				---		83	1	83(CYS)
	24										GLN				---		75	5	43(ARG)
	25										ALA				---		75	4	71(ALA)
	26										SER				---		72	4	67(SER)
	27										GLN				---		72	4	66(GLN) : 53(GLN)
	27A										---				---		4	2	3(SER)
	27B										---				---		4	2	3(VAL)
CDR1	27C										---				---		2	2	1(+)
CDR1	27D										---				---		2	2	1(+)
CDR1	27E										---				---		1	1	1(SER)
CDR1	27F										---				---				
CDR1	28										ASP				---		72	8	25(ASP) : 22(SER)
	29										ILE				---		71	5	61(ILE)
	30										ASN				---		68	10 : 11	35(SER)
	31										LYS				---		66	10	24(SER)
	32														---		66	7	33(TYR)
	33														---		64	4	60(LEU)
	34														---		60	7 : 8	24(ASN) : 22(ALA)
	35														---		63	1	63(TRP)
	36														---		61	2	57(TYR)
	37														---		60	4	56(GLN) : 49(GLN)
	38														---		58	4	55(GLN) : 50(GLN)
	39														---		55	4	50(LYS)
	40														---		57	4	54(PRO)
FR2	41														---		44	3	40(GLY)
FR2	42														---		46	5	35(LYS)
FR2	43														---		47	2	42(ALA)
	44														---		47	1	47(PRO)
	45														---		47	6	41(LYS)
	46														---		46	7	33(LEU)
	47														---		45	2	44(LEU)
	48														---		43	2	42(ILE)
	49														---		45	4	42(TYR)
	50														---		45	7 : 8	15(+)
	51														---		45	5	39(ALA)
CDR2	52														---		44	4	41(SER)
CDR2	53														---		43	5 : 6	18(SER)
	54														---		44	2	43(LEU)
	55														---		44	7	20(GLU)
	56														---		42	7	27(SER)
	57														---		43	1	43(GLY)
	58														---		43	2	42(VAL)
	59														---		42	4	39(PRO)
	60														---		42	1	42(SER)
	61														---		43	3	41(ARG)
	62														---		43	3	41(PHE)
	63														---		43	7	36(SER)
	64														---		43	1	43(GLY)
	65														---		42	4	38(SER)
	66														---		43	3	41(GLY)
	67														---		41	3	38(SER)
	68														---		41	3	38(GLY)
	69														---		41	3	38(THR)
	70														---		41	5 : 6	25(ASP) : 23(ASP)
FR3	71														---		40	4	36(PHE)
FR3	72														---		40	4	37(THR)
FR3	73														---		40	3	31(LEU)
	74														---		40	4	37(THR)
	75														---		40	3	38(ILE)
	76														---		39	2	37(SER)
	77														---		40	5	27(SER)
	78														---	LEU	40	2	35(LEU)
	79														---	GLN	40	2 : 3	39(GLN) : 35(GLN)
	80														---	PRO	40	3	33(PRO)
	81														---	GLU	40	3 : 5	29(GLU) : 26(GLU)
	82														---	ASP	40	1 : 2	40(ASP) : 37(ASP)
	83														---	PHE	40	4	28(PHE)
	84														---	ALA	40	2	39(ALA)
	85														---	THR	40	4	37(THR)
	86										TYR				---	TYR	42	2	41(TYR)
	87										TYR				---	TYR	41	2	40(TYR)
	88										CYS				---	CYS	42	1	42(CYS)
	89										GLN				---	GLN	43	3 : 4	40(GLN) : 37(GLN)
	90										GLN				---	GLN	43	3 : 4	39(GLN) : 34(GLN)
	91										TYR				---	HIS	45	10 : 11	24(TYR)
	92										GLU				ASP	ASP	46	8	15(ASN) : 13(+)
	93										ASN				ILE	HIS	46	9	20(SER)
	94										LEU				PHE	LEU	46	10	12(LEU)
CDR3	95										PRO				PRO	PRO	45	5	35(PRO)
CDR3	95A										---				---	---	5	3	2(+)
CDR3	95B										---				---	---	4	2	2(+)
CDR3	95C										---				---	---	4	3	2(TYR)
CDR3	95D										---				---	---	1	1	1(ASP)
CDR3	95E										---				---	---			
CDR3	95F										---				---	---			
CDR3	96										TYR				GLY	LEU	32	12	9(TYR)
CDR3	97														THR	THR	31	4	27(THR)
	98														PHE	PHE	31	3	29(PHE)
	99														GLY	GLY	31	1	31(GLY)
	100														GLN	GLY	31	4 : 5	18(GLN) : 17(GLN)
	101														GLY	GLY	31	1	31(GLY)
	102														THR	THR	31	2	30(THR)
FR4	103														LYS	THR	31	4	23(LYS)
FR4	104														VAL	VAL	30	2	23(VAL)
FR4	105														GLU	GLU	30	3 : 4	20(GLU) : 19(GLU)
FR4	106														ILE	MET	31	7	15(ILE)
FR4	106A														---	---			
FR4	107														LYS	LYS	31	2	29(LYS)
	108														ARG	ARG	24	2	22(ARG)
	109														THR	THR	20	1	20(THR)

HUMAN KAPPA LIGHT CHAINS SUBGROUP I (cont'd)

VARIABILITY

	0	
	1	3.2 : 4.4
	2	4.2
	3	8.9 : 9.3
	4	4.6
	5	3.1
	6	1. : 2.1
	7	3.2
	8	3.1
	9	4.2
FR1	10	6.4
FR1	11	5.7
FR1	12	4.2
FR1	13	4.4
FR1	14	7.9
	15	3.1
	16	2.
	17	3.2 : 4.7
	18	6.6
	19	3.1
	20	4.2
	21	4.2
	22	8.2
	23	1.
	24	8.7
	25	4.2
	26	4.3
	27	4.4 : 5.4
	27A	
	27B	
CDR1	27C	
CDR1	27D	
CDR1	27E	
CDR1	27F	
CDR1	28	23. : 26.
	29	5.8
	30	19. : 21.
	31	28.
	32	14.
	33	4.3
	34	18. : 22.
	35	1.
	36	2.1
	37	4.3 : 4.9
	38	4.2 : 4.6
	39	4.4
	40	4.2
FR2	41	3.3
FR2	42	6.6
FR2	43	2.2
	44	1.
	45	6.9
	46	9.8
	47	2.
	48	2.
	49	4.3
	50	21. : 24.
	51	5.8
	52	4.3
CDR2	53	12. : 14.
CDR2	54	2.
CDR2	55	15.
CDR2	56	11.
	57	1.
	58	2.
	59	4.3
	60	1.
	61	3.1
	62	3.1
	63	8.4
	64	1.
	65	4.4
	66	3.1
	67	3.2
	68	3.2
	69	3.2
	70	8.2 : 11.
	71	4.4
FR3	72	4.3
FR3	73	3.9
	74	4.3
	75	3.2
	76	2.1
	77	7.4
	78	2.3
	79	2.1 : 3.4
	80	3.6
	81	4.1 : 7.7
	82	1. : 2.2
	83	5.7
	84	2.1
	85	4.3
	86	2.
	87	2.1
	88	1.
	89	3.2 : 4.6
	90	3.3 : 5.1
	91	19. : 21.
	92	25. : 28.
	93	21.
	94	38.
CDR3	95	6.4
CDR3	95A	
CDR3	95B	
CDR3	95C	
CDR3	95D	
CDR3	95E	
CDR3	95F	
CDR3	96	43.
CDR3	97	4.6
	98	3.2
	99	1.
	100	6.9 : 9.1
	101	1.
FR4	102	2.1
FR4	103	5.4
FR4	104	2.6
FR4	105	4.5 : 6.3
FR4	106	14.
FR4	106A	
FR4	107	2.1
FR4	108	2.2
FR4	109	1.

ANTIBODY SPECIFICITIES: HUMAN KAPPA LIGHT CHAINS SUBGROUP I

8) **WEA:** ANTI-3,4-PYRUVYLATED GALACTOSE MONOCLONAL
25) **LOW:** COLD AGGLUTININ WITH ANTI-BLOOD GROUP I ACTIVITY
39) **LAY:** ANTI-HUMAN GAMMA G1 AND G3 GLOBULINS; PO IDIOTYPE
53) **HEI:** COLD AGGLUTININ WITH ANTI-GD (MEMBRANE-GLYCOLIPID-DEPENDENT) ACTIVITY
66) **DAV:** ANTI-HUMAN GAMMA G GLOBULIN
67) **FIN:** ANTI-HUMAN GAMMA G GLOBULIN
92) **WAG:** ANTI-DINITROPHENYL
104) **MAR:** ANTI-LIPOPROTEIN LIPASE

ALLOTYPE: HUMAN KAPPA LIGHT CHAINS SUBGROUP I

79) **KUE:** INV(2)

CLASS: HUMAN KAPPA LIGHT CHAINS SUBGROUP I

8) **WEA:** IGM-KAPPA
33) **F-GUI:** IGG3-KAPPA
55) **S-GUI:** IGG3-KAPPA
74) **PW:** IGG1-KAPPA
82) **RI:** IGG1-KAPPA

REFERENCE: HUMAN KAPPA LIGHT CHAINS SUBGROUP I

1) **ROY:** HILSCHMANN,N. & CRAIG,L.C. (1965) PROC.NAT.ACAD.SCI.USA,53,1403-1409; HILSCHMANN,N. (1967) Z.PHYSIOL.CHEM.,348,1077-1080; HILSCHMANN,N.,BARNIKOL,H.U.,HESS,M.,LANGER,B.,PONSTINGL,H.,STEINMETZ-KAYNE,M.,SUTER,L. & WATANABE,S. (1969) PROC. 5TH FEBS SYMP., 15,57-74. (CHECKED BY AUTHOR WHO PROVIDED ADDITIONAL RESIDUES TO THOSE PUBLISHED AND CORRECTED RESIDUES 65 AND 67 AS GIVEN IN THE TABLE)
2) **AU:** SCHIECHL,H. & HILSCHMANN,N. (1971) Z.PHYSIOL.CHEM.,352,111-115; (1972) Z.PHYSIOL.CHEM.,353,345-370. (CHECKED BY AUTHOR)
3) **REI:** PALM,W. & HILSCHMANN,N. (1973) Z.PHYSIOL.CHEM.,354,1651-1654; (1975) Z.PHYSIOL.CHEM.,356,167-191. (CHECKED BY AUTHOR)
4) **HAU:** WATANABE,S. & HILSCHMANN,N. (1970) Z.PHYSIOL.CHEM.,351,1291-1295. (CHECKED BY AUTHOR)
5) **HK101'CL:** BENTLEY,D.L. & RABBITTS,T.H. (1980) NATURE,288,730-733. (CHECKED BY AUTHOR 11/30/82)
6) **SCW:** EULITZ,M.,GOTZE,D. & HILSCHMANN,N. (1972) Z.PHYSIOL.CHEM.,353,487-491; EULITZ,M. & HILSCHMANN,N. (1974) Z.PHYSIOL.CHEM.,355,842-866. (CHECKED BY AUTHOR)
7) **AG:** TITANI,K.,SHINODA,T. & PUTNAM,F.W. (1969) J.BIOL.CHEM.,244,3550-3560. (CHECKED BY AUTHOR 06/15/83)
8) **WEA:** GONI,F. & FRANGIONE,B. (1983) PROC.NAT.ACAD.SCI.USA,80,4837-4841. (CHECKED BY AUTHOR 03/23/84)
9) **HK137'CL:** BENTLEY,D.L. & RABBITTS,T.H. (1983) CELL,32,181-189.
10) **HK134'CL:** BENTLEY,D.L. & RABBITTS,T.H. (1983) CELL,32,181-189.
11) **DAUDI'CL:** KLOBECK,H.G.,COMBRIATO,G. & ZACHAU,H.G. (1984) NUC.ACIDS RES.,12,18,6995-7006.
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13) **HF3-16/6:** ATKINSON,P.M.,LAMPMAN,G.W.,FURIE,B.C.,NAPARSTEK,Y.,SCHWARTZ,R.S.,STOLLAR,B.D. & FURIE,B. (1985) J.CLIN.INVEST.,75,1138-1143. (CHECKED BY AUTHOR 08/21/85)
14) **HF2-1/13B:** ATKINSON,P.M.,LAMPMAN,G.W.,FURIE,B.C.,NAPARSTEK,Y.,SCHWARTZ,R.S.,STOLLAR,B.D. & FURIE,B. (1985) J.CLIN.INVEST.,75,1138-1143. (CHECKED BY AUTHOR 08/21/85)
15) **HF2-18/2:** ATKINSON,P.M.,LAMPMAN,G.W.,FURIE,B.C.,NAPARSTEK,Y.,SCHWARTZ,R.S.,STOLLAR,B.D. & FURIE,B. (1985) J.CLIN.INVEST.,75,1138-1143. (CHECKED BY AUTHOR 08/21/85)
16) **HF2-1/17:** ATKINSON,P.M.,LAMPMAN,G.W.,FURIE,B.C.,NAPARSTEK,Y.,SCHWARTZ,R.S.,STOLLAR,B.D. & FURIE,B. (1985) J.CLIN.INVEST.,75,1138-1143. (CHECKED BY AUTHOR 08/21/85)
17) **BJ26:** ALESCIO-ZONTA,L. & BAGLIONI,C. (1970) EUR.J.BIOCHEM.,15,450-463. (CHECKED BY AUTHOR)
18) **RFZ:** SMITHIES,O.,GIBSON,D.,FANNING,E.M.,GOODFLIESH,R.M.,GILMAN,J.G. & BALLANTYNE,D.L. (1971) BIOCHEMISTRY,10,4912-4921. (CHECKED BY AUTHOR)
19) **PSM:** SEON,B.K. (1982) MOL.IMMUNOL.,19,83-86. (CHECKED BY AUTHOR 05/23/83)
20) **HOM:** CAVVIDOU,G.,KLEIN,M.,HORNE,C.,HOFMANN,T. & DORRINGTON,K.J. (1981) MOL.IMMUNOL.,18,793-805.
21) **ESM IGG:** KUAN,T.K.,TUNG,E.,WANG,I.Y. & WANG,A.C. (1981) IMMUNOL.,44,265-271. (CHECKED BY AUTHOR 05/26/83)
22) **ESM IGM:** KUAN,T.K.,TUNG,E.,WANG,I.Y. & WANG,A.C. (1981) IMMUNOL.,44,265-271. (CHECKED BY AUTHOR 05/26/83)
23) **WAT:** STEVENS,F.J.,WESTHOLM,F.A.,PANAGIOTOPOULOS,N.,SCHIFFER,M.,POPP,R.A. & SOLOMON,A. (1981) J.MOL.BIOL.,147,185-193. (CHECKED BY AUTHOR 05/26/1983)
24) **AMYLOID VIII-B:** GLENNER,G.G.,TERRY,W.,HERADA,M.,ISERSKY,C. & PAGE,D. (1971) SCIENCE,172,1150-1151. (CHECKED BY AUTHOR 09/22/78)
25) **LOW:** CAPRA,J.D.,KEHOE,J.M.,WILLIAMS,R.C.,JR.,FEIZI,T. & KUNKEL,H.G. (1972) PROC.NAT.ACAD.SCI.USA,69,40-43. (CHECKED BY AUTHOR WHO CORRECTED RESIDUE 16 AS GIVEN IN TABLE)
26) **DIE:** CAPRA,J.D. & KUNKEL,H.G. (1970) PROC.NAT.ACAD.SCI.USA,67,87-92. (CHECKED BY AUTHOR)
27) **CAR A:** CAPRA,J.D. & KUNKEL,H.G. (1970) PROC.NAT.ACAD.SCI.USA,67,87-92. (CHECKED BY AUTHOR)
28) **TEI:** CAPRA,J.D. & KUNKEL,H.G. (1970) PROC.NAT.ACAD.SCI.USA,67,87-92. (CHECKED BY AUTHOR)
29) **BJ48:** ALESCIO-ZONTA,L. & BAGLIONI,C. (1970) EUR.J.BIOCHEM.,15,450-463. (CHECKED BY AUTHOR)
30) **CON:** NIALL,H.D. & EDMAN,P. (1967) NATURE,216,262-263. (CHECKED BY AUTHOR 07/25/79)
31) **TRA:** NIALL,H.D. & EDMAN,P. (1967) NATURE,216,262-263. (CHECKED BY AUTHOR 07/25/79)
32) **AMYLOID LEP:** LIAN,J.B.,SKINNER,M.,BENSON,M.D. & COHEN,A.S. (1977) BIOCHIM.BIOPHYS.ACTA,491,167-176.
33) **F-GUI:** WANG,A.C.,FUDENBERG,H.H. & CREYSSEL,R. (1982) ACTA HAEMAT.,68,187-195. (CHECKED BY AUTHOR 05/26/83)
34) **OU(IOC):** KOHLER,H.,SHIMIZU,A.,PAUL,C. & PUTNAM,F.W. (1970) SCIENCE,169,56-59. (KAPLAN,A.P. & METZGER,H. (1969) BIOCHEMISTRY,8,3944-3951.) (CHECKED BY AUTHOR 06/15/83)
35) **DEE:** MILSTEIN,C. & DEVERSON,E.V. (1971) BIOCHEM.J.,123,945-958. (CHECKED BY AUTHOR)
36) **GAL(I):** LAURE,C.J.,WATANABE,S. & HILSCHMANN,N. (1973) Z.PHYSIOL.CHEM.,354,1503-1504. (CHECKED BY AUTHOR)
37) **JOH:** CAPRA,J.D. & KUNKEL,H.G. (1970) PROC.NAT.ACAD.SCI.USA,67,87-92. (CHECKED BY AUTHOR)
38) **KER:** MILSTEIN,C. (1966) BIOCHEM.J.,101,352-368. (CHECKED BY AUTHOR WHO PROVIDED ADDITIONAL RESIDUES TO THOSE PUBLISHED)
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40) **BRA:** WANG,A.C.,WELLS,J.V.,FUDENBERG,H.H. & GERGELY,J. (1974) IMMUNOCHEM.,11,341-345. (CHECKED BY AUTHOR)
41) **WES:** KRATZIN,H.,YANG,C.Y.,KRUSCHE,J.U. & HILSCHMANN,N. (1980) Z.PHYSIOL.CHEM.,361,1591-1598.
42) **Vb'CL:** PECH,M.,JAENICHEN,H.-R.,POHLENZ,H.-D.,NEUMAIER,P.S.,KLOBECK,H.-G. & ZACHAU,H.G. (1984) J.MOL.BIOL.,176,189-204. (CHECKED BY AUTHOR 12/14/84)
43) **Vb''CL:** PECH,M.,JAENICHEN,H.-R.,POHLENZ,H.-D.,NEUMAIER,P.S.,KLOBECK,H.-G. & ZACHAU,H.G. (1984) J.MOL.BIOL.,176,189-204. (CHECKED BY AUTHOR 12/14/84)
44) **HK102'CL:** BENTLEY,D.L. & RABBITTS,T.H. (1980) NATURE,288,730-733. (CHECKED BY AUTHOR 11/30/82)
45) **EU:** GOTTLIEB,P.D.,CUNNINGHAM,B.A.,RUTISHAUSER,U. & EDELMAN,G.M. (1970) BIOCHEMISTRY,9,3155-3161. (CHECKED BY AUTHOR)
46) **DEN:** YANG,C.Y.,PAULY,E.,KRATZIN,H. & HILSCHMANN,N. (1981) Z.PHYSIOL.CHEM.,362,1131-1146.
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49) **FRA:** MEINKE,G.C.,SIGRIST,P.H. & SPIEGELBERG,H.L. (1974) IMMUNOCHEM.,11,457-460. (CHECKED BY AUTHOR WHO PROVIDED ADDITIONAL RESIDUES TO THOSE PUBLISHED); MEINKE,G.C. & SPIEGELBERG,H.L. (1976) IMMUNOCHEM.,13,915-919. (CHECKED BY AUTHOR 10/17/77)
50) **GR':** FAIR,D.S.,SLEDGE,C.,KRUEGER,R.G.,MANN,K.G. & HOOD,L.E. (1975) BIOCHEMISTRY,14,5561-5568.
51) **PAUL:** SMITH,G.P.,HOOD,L. & FITCH,W.M. (1971) ANN.REV.BIOCHEM.,40,969-1012.
52) **MON:** NIALL,H.D. & EDMAN,P. (1967) NATURE,216,262-263. (CHECKED BY AUTHOR 07/25/79)
53) **HEI:** RIESEN,W.F.,MAJANIEMI,I.,HUSER,H.,BRAUN,D.G. & ROELCKE,D. (1978) SCAND.J.IMMUNOL.,8,145-148. (CHECKED BY AUTHOR 10/10/79)
54) **POT:** CAPRA,J.D. & KUNKEL,H.G. (1970) PROC.NAT.ACAD.SCI.USA,67,87-92. (CHECKED BY AUTHOR WHO CORRECTED RESIDUE 9 AS GIVEN IN TABLE)
55) **S-GUI:** WANG,A.C.,FUDENBERG,H.H. & CREYSSEL,R. (1982) ACTA HAEMAT.,68,187-195. (CHECKED BY AUTHOR 05/26/83)
56) **AMYLOID BAN:** DWULET,F.E.,O'CONNOR,T.P. & BENSON,M.D. (1986) MOL.IMMUNOL.,23,73-78.
57) **BJ19:** ALESCIO-ZONTA,L. & BAGLIONI,C. (1970) EUR.J.BIOCHEM.,15,450-463. (CHECKED BY AUTHOR)
58) **BEL:** MILSTEIN,C. (1969) PROC. 5TH FEBS SYMP.,15,43-56. (CHECKED BY AUTHOR WHO PROVIDED ADDITIONAL RESIDUES TO THOSE PUBLISHED AND CORRECTED RESIDUES 1,3,6,27,79 AND 82 AS GIVEN IN TABLE)
59) **JBL:** SEON,B.K. (1982) MOL.IMMUNOL.,19,83-86. (CHECKED BY AUTHOR 05/23/83)
60) **PAP:** NIALL,H.D. & EDMAN,P. (1967) NATURE,216,262-263. (CHECKED BY AUTHOR 07/25/79)
61) **CAR:** MILSTEIN,C.P. & DEVERSON,E.V. (1974) EUR.J.BIOCHEM.,49,377-391. (CHECKED BY AUTHOR)
62) **MEV:** EULITZ,M. & LINKE,R.P. (1982) Z.PHYSIOL.CHEM.,363,1347-1358. (CHECKED BY AUTHOR 10/10/83)

REFERENCE: HUMAN KAPPA LIGHT CHAINS SUBGROUP I (cont'd)

63) **BI:** BRAUN,H.,LEIBOLD,W.,BARNIKOL,H.U. & HILSCHMANN,N. (1971) Z.PHYSIOL.CHEM.,352,647-651; (1972) Z.PHYSIOL.CHEM.,353,1284-1306. (CHECKED BY AUTHOR WHO PROVIDED AN ADDITIONAL RESIDUE TO THOSE PUBLISHED AND CORRECTED RESIDUE 72 AS GIVEN IN TABLE)

64) **AMYLOID ES305:** WESTERMARK,P.,SLETTEN,K. & NATVIG,J.B. (1981) ACTA PATH.MICROBIOL.SCAND.,C89,199-203. (CHECKED BY AUTHOR 11/09/81)

65) **CRA:** NIALL,H.D. & EDMAN,P. (1967) NATURE,216,262-263. (CHECKED BY AUTHOR 07/25/79)

66) **DAV:** CAPRA,J.D. & KUNKEL,H.G. (1970) PROC.NAT.ACAD.SCI.USA,67,87-92. (CHECKED BY AUTHOR)

67) **FIN:** CAPRA,J.D. & KUNKEL,H.G. (1970) PROC.NAT.ACAD.SCI.USA,67,87-92. (CHECKED BY AUTHOR)

68) **KA:** SHINODA,T. (1975) J.BIOCHEM.,77,1277-1296. (CHECKED BY AUTHOR)

69) **Vd'CL:** PECH,M.,JAENICHEN,H.-R.,POHLENZ,H.-D.,NEUMAIER,P.S.,KLOBECK,H.-G. & ZACHAU,H.G. (1984) J.MOL.BIOL.,176,189-204. (CHECKED BY AUTHOR 12/14/84)

70) **LUX:** NIALL,H.D. & EDMAN,P. (1967) NATURE,216,262-263. (CHECKED BY AUTHOR 07/25/79)

71) **NE:** MATTHEWS,J.B. & JEFFERIS,R. (1977) IMMUNOCHEM.,14,793-797. (CHECKED BY AUTHOR 08/10/79)

72) **Va''CL:** PECH,M.,JAENICHEN,H.-R.,POHLENZ,H.-D.,NEUMAIER,P.S.,KLOBECK,H.-G. & ZACHAU,H.G. (1984) J.MOL.BIOL.,176,189-204. (CHECKED BY AUTHOR 12/14/84)

73) **NI:** SHINODA,T. (1973) J.BIOCHEM.,73,433-446. (CHECKED BY AUTHOR)

74) **FW:** PICK,A.I.,WANG,A.C.,FROHLICHMAN,R. & FUDENBERG,H.H. (1982) ACTA HAEMAT.,68,207-214. (CHECKED BY AUTHOR 05/26/83)

75) **AMYLOID X:** GLENNER,G.G.,TERRY,W.,HERADA,M.,ISERSKY,C. & PAGE,D. (1971) SCIENCE,172,1150-1151. (CHECKED BY AUTHOR 09/22/78)

76) **ALE:** MILSTEIN,C.,MILSTEIN,C.P.& FEINSTEIN,A. (1969) NATURE,221,151-154. (CHECKED BY AUTHOR)

77) **CHE:** MEINKE,G.C. & SPIEGELBERG,H.L. (1976) IMMUNOCHEM.,13,915-919. (CHECKED BY AUTHOR 10/17/77)

78) **ADA:** MEINKE,G.C. & SPIEGELBERG,H.L. (1976) IMMUNOCHEM.,13,915-919. (CHECKED BY AUTHOR 10/17/77)

79) **KUE:** EULITZ,M.,KLEY,H.P. & ZEITLER,H.J. (1979) Z.PHYSIOL.CHEM.,360,725-734. (CHECKED BY AUTHOR 07/17/79)

80) **GO:** WANG,A.C.,FUDENBERG,H.H. & CREYSSEL,R. (1974) EUR.J.IMMUNOL.,4,446-448. (CHECKED BY AUTHOR)

81) **BOL:** WANG,A.C.,WELLS,J.V.,FUDENBERG,H.H. & GERGELY,J. (1974) IMMUNOCHEM.,11,341-345. (CHECKED BY AUTHOR)

82) **RI:** PICK,A.I.,WANG,A.C.,FROHLICHMAN,R. & FUDENBERG,H.H. (1982) ACTA HAEMAT.,68,207-214. (CHECKED BY AUTHOR 05/26/83)

83) **Ve'CL:** PECH,M.,JAENICHEN,H.-R.,POHLENZ,H.-D.,NEUMAIER,P.S.,KLOBECK,H.-G. & ZACHAU,H.G. (1984) J.MOL.BIOL.,176,189-204. (CHECKED BY AUTHOR 12/14/84)

84) **OCO:** WANG,A.C.,WELLS,J.V.,FUDENBERG,H.H. & GERGELY,J. (1974) IMMUNOCHEM.,11,341-345. (CHECKED BY AUTHOR)

85) **V13'CL:** JAENICHEN,H.-R.,PECH,M.,LINDENMAIER,W.,WILDGRUBER,N. & ZACHAU,H.G. (1984) NUC.ACIDS RES.,12,5249-5263. (CHECKED BY AUTHOR 12/14/84)

86) **V18A'CL:** HEIDMANN,O. & ROUGEON,F. (1984) NATURE,311,74-76.

87) **V19A'CL:** HEIDMANN,O. & ROUGEON,F. (1984) NATURE,311,74-76.

88) **V19B'CL:** HEIDMANN,O. & ROUGEON,F. (1984) NATURE,311,74-76.

89) **V18B'CL:** HEIDMANN,O. & ROUGEON,F. (1984) NATURE,311,74-76.

90) **HF6-21/28:** ATKINSON,P.M.,LAMPMAN,G.W.,FURIE,B.C.,NAPARSTEK,Y.,SCHWARTZ,R.S.,STOLLAR,B.D. & FURIE,B. (1985) J.CLIN.INVEST.,75,1138-1143. (CHECKED BY AUTHOR 08/21/85)

91) **SAC:** SMITHIES,O.,GIBSON,O.M.,FANNING,E.M.,PERCY,M.E.,PARR,D.M. & CONNELL,G.E. (1971) SCIENCE,172,574-577. (CHECKED BY AUTHOR)

92) **WAG:** KAPLAN,A.P. & METZGER,H. (1969) BIOCHEMISTRY,8,3944-3951. (CHECKED BY AUTHOR)

93) **HBJ1:** HOOD,L.,GRAY,W.R.,SANDERS,B.G. & DREYER,W.J. (1967) COLD SPRING HARBOR SYMP. QUANTITATIVE BIOL.,32,133-145.

94) **AMYLOID 547:** WESTERMARK,P.,SLETTEN,K. & NATVIG,J.B. (1981) ACTA PATH.MICROBIOL.SCAND.,C89,199-203. (CHECKED BY AUTHOR 11/09/81)

95) **WEB:** JOHNSTON,S.L.,ABRAHAM,G.N. & WELCH,E.H. (1975) BIOCHEM.BIOPHYS.RES.COMMUN.,66,842-847. (CHECKED BY AUTHOR 10/17/77)

96) **HOE:** JOHNSTON,S.L.,ABRAHAM,G.N. & WELCH,E.H. (1975) BIOCHEM.BIOPHYS.RES.COMMUN.,66,842-847. (CHECKED BY AUTHOR 10/17/77)

97) **LOD:** JOHNSTON,S.L.,ABRAHAM,G.N. & WELCH,E.H. (1975) BIOCHEM.BIOPHYS.RES.COMMUN.,66,842-847. (CHECKED BY AUTHOR 10/17/77)

98) **HBJ10:** HOOD,L.,GRAY,W.R.,SANDERS,B.G. & DREYER,W.J. (1967) COLD SPRING HARBOR SYMP. QUANTITATIVE BIOL.,32,133-145.

99) **BEN:** CAPRA,J.D.,KEHOE,J.M.,WILLIAMS,R.C.,JR.,FEIZI,T. & KUNKEL,H.G. (1972) PROC.NAT.ACAD.SCI.USA,69,40-43. (CHECKED BY AUTHOR)

100) **GR:** CAPRA,J.D.,KEHOE,J.M.,WILLIAMS,R.C.,JR.,FEIZI,T. & KUNKEL,H.G. (1972) PROC.NAT.ACAD.SCI.USA,69,40-43. (CHECKED BY AUTHOR)

101) **MAA:** CAPRA,J.D.,KEHOE,J.M.,WILLIAMS,R.C.,JR.,FEIZI,T. & KUNKEL,H.G. (1972) PROC.NAT.ACAD.SCI.USA,69,40-43. (CHECKED BY AUTHOR)

102) **MUK:** LITMAN,G.W.,GERBER-JENSON,B.,LITMAN,R.,MIDDAUGH,C.R. & SCHEFFEL,C. (1980) MOL.IMMUNOL.,17,337-344.

103) **AMYLOID 594:** WESTERMARK,P.,SLETTEN,K. & NATVIG,J.B. (1981) ACTA PATH.MICROBIOL.SCAND.,C89,199-203. (CHECKED BY AUTHOR 11/09/81)

104) **MAR:** KAPLAN,A.P. & METZGER,H. (1969) BIOCHEMISTRY,8,3944-3951. (CHECKED BY AUTHOR)

105) **AMYLOID:** COHEN,A.S.,SHIRAHAMA,T.,SKINNER,M.,BENSON,M.D. & CATHCART,E.S. (1973) PROTIDES BIOL.FLUIDS,20,73-80.

106) **BJ:** MILSTEIN,C. (1966) BIOCHEM.J.,101,352-368. (CHECKED BY AUTHOR)

107) **HBJ6:** HOOD,L.,GRAY,W.R.,SANDERS,B.G. & DREYER,W.J. (1967) COLD SPRING HARBOR SYMP. QUANTITATIVE BIOL.,32,133-145.

108) **PEN:** MOULIN,A. & FOUGEREAU,M. (1973) NATURE NEW BIOLOGY,246,176-178.

109) **AMYLOID MS:** PICK,A.I.,SCHREIBMAN,S.,LAVIE,G. & FROHLICHMAN,R. (1973) PROTIDES BIOL.FLUIDS,20,63-72.

110) **CL*:** SOLOMON,A.,MCLAUGHLIN,C.L. & CAPRA,J.D. (1975) J.CLINICAL INVESTIGATION,55,579-586. (CHECKED BY AUTHOR)

111) **GM131'CL:** MORIN,J.W.,BLACK,A.,WU,M. & BEYCHOK,S. (1985) PROC.NAT.ACAD.SCI.USA,82,7025-7029.

NOTES: HUMAN KAPPA LIGHT CHAINS SUBGROUP I

IDENTICAL SETS OF FRAMEWORK SEGMENTS:

FR1:
- SET 1: ROY[1],AU[2],REI[3],HAU[4],HK101'CL[5],SCW[6],AG[7],WEA[8],HK137'CL[9],HK134'CL[10],DAUDI'CL[11],WALKER'CL[12], HF3-16/6[13],HF2-1/13B[14],HF2-18/2[15],HF2-1/17[16],BJ26[17],RFZ[18],PSM[19],HOM[20],ESM IGG[21],ESM IGM[22],WAT[23], AMYLOID VIII-B[24],LOW[25],DIE[26],CAR A[27],TEI[28],BJ48[29],CON[30],TRA[31],F-GUI[33],OU(IOC)[34],DEE[35]. (34 IDENTICAL)
- SET 2: WES[41],Vb'CL[42],Vb''CL[43]. (3 IDENTICAL)
- SET 3: HK102'CL[44],EU[45],DEN[46],PAU[47],HBJ4[48],FRA[49],GR'[50],PAUL[51],MON[52]. (9 IDENTICAL)
- SET 4: AMYLOID BAN[56],BJ19[57],BEL[58]. (3 IDENTICAL)
- SET 5: DAV[66],FIN[67]. (2 IDENTICAL)
- SET 6: Vd'CL[69],LUX[70]. (2 IDENTICAL)

FR2:
- SET 1: ROY[1],AU[2],WALKER'CL[12],Vb'CL[42],Vb''CL[43],HK102'CL[44],KA[68],Vd'CL[69],Va''CL[72],Ve'CL[83]. (10 IDENTICAL)
- SET 2: HK101'CL[5],HK134'CL[10]. (2 IDENTICAL)
- SET 3: HK137'CL[9],AMYLOID BAN[56]. (2 IDENTICAL)
- SET 4: V18A'CL[86]. (IDENTICAL TO 7 MOUSE V-KAPPA-III: PC1229(NZB)[1],PC2880(NZB)[2],PC7132(NZB)[3],MOPC70[5],PC2413(NZB)[11], 50S10.1[27],V-21B18KB'CL[46]; AND 5 RABBIT V-KAPPA: K9-335[1],K9-338[2],K29-213[3],V20'CL[36],K18-167[64].)
- SET 5: V19B'CL[88],V18B'CL[89]. (2 IDENTICAL HUMAN V-KAPPA-I; ALSO 4 HUMAN V-KAPPA-IV: VJI'CL[1],VKAPPA IV GERMLINE'CL[2], PB17IV'CL[3],LEN[4]; 1 MOUSE V-KAPPA-I: MCPC603[47]; 30 MOUSE V-KAPPA-III: MPC11'CL[6],TEPC111[7],PC3741(NZB)[8], TEPC124[9],MOPC321[12],PC7043(NZB)[13],PC7183(NZB)[14],PC6308(NZB)[15],PC6684(NZB)[17],PC7940(NZB)[18],PC7175(NZB)[19], PC2485(NZB)[20],PC4039(NZB)[21],PC7210(NZB)[23],H36-15[26],2242[29],V-21E1.5KB'CL[30],V-21C9.5KB'CL[31], PC7461(NZB)[33],PC2960(NZB)[34],97.C(A.BY)[35],10.A(A.TH)[39],H36-5[48],40.C(A.TH)[52],MOPC63[54],ABPC22[55], PC9245(NZB)[56],PC4050(NZB)[57],V-21B16KB'CL[58],11949[62]; 1 MOUSE V-KAPPA-VI: BFPC61A'CL[64]; AND 15 RABBIT V-KAPPA: K9-335-I[19],3368[20],BS-5[38],BS-1[39],K49-501[45],3547[47],K4820[57],K30-267[61],311[65],4422[66],17D9'CL[68], 4192[71],4363[85],120[103],K-25[112].)

FR3:
- SET 1: HAU[4],HK101'CL[5],HK137'CL[9],HK134'CL[10],Vb'CL[42],Vb''CL[43],Va''CL[72]. (7 IDENTICAL)
- SET 2: Ve'CL[83],V13'CL[85]. (2 IDENTICAL)
- SET 3: V19B'CL[88],V18B'CL[89]. (2 IDENTICAL)

FR4:
- SET 1: AU[2],GAL(I)[36],CL*[110]. (3 IDENTICAL HUMAN V-KAPPA-I; ALSO 2 HUMAN V-KAPPA-II: GM 607 'CL[5],RPM1-6410'CL[16]; 7 HUMAN V-KAPPA-III: WOL[2],PAY[7],PIE[11],GLO[15],CUR[20],REE[57],VKAPPA3'CL[82]; AND 1 HUMAN V-KAPPA-IV: PB17IV'CL[3].)
- SET 2: HAU[4]. (IDENTICAL TO 1 HUMAN V-KAPPA-III: POM[48].)
- SET 3: AG[7],DEN[46],BI[63]. (3 IDENTICAL HUMAN V-KAPPA-I; ALSO 2 HUMAN V-KAPPA-II: NIM[3],FR[14]; 6 HUMAN V-KAPPA-III: NEU[5], GOT[6],GAR'[10],FLO[12],FR4[21],IARC/BL41'CL[28]; AND 1 HUMAN V-KAPPA-IV: LEN[4].)
- SET 4: WEA[8],BJ48[29],LAY[39],EU[45]. (4 IDENTICAL)
- SET 5: WALKER'CL[12],OU(IOC)[34]. (2 IDENTICAL HUMAN V-KAPPA-I; ALSO 1 HUMAN V-KAPPA-II: TEW[1].)
- SET 6: WES[41],MEV[62]. (2 IDENTICAL)

IDENTICAL SETS OF COMPLEMENTARITY DETERMINING REGIONS:

CDR1:
- SET 1: AU[2],NE[71],SHE[77]. (3 IDENTICAL)
- SET 2: WEA[8],GAL(I)[36]. (2 IDENTICAL)
- SET 3: HK134'CL[10],Vb'CL[42],Vb''CL[43]. (3 IDENTICAL)
- SET 4: HF3-16/6[13],HF2-1/13B[14],HF2-18/2[15],HF2-1/17[16]. (4 IDENTICAL)
- SET 5: Vd'CL[69],Ve'CL[83]. (2 IDENTICAL)

CDR2:
- SET 1: HK101'CL[5],HK137'CL[9],HK134'CL[10],WALKER'CL[12],Vb'CL[42],Vb''CL[43]. (6 IDENTICAL)
- SET 2: AG[7],NI[73]. (2 IDENTICAL)
- SET 3: HK102'CL[44],Va''CL[72]. (2 IDENTICAL)
- SET 4: Vd'CL[69],Ve'CL[83],V13'CL[85]. (3 IDENTICAL)
- SET 5: V18A'CL[86]. (IDENTICAL TO 1 RABBIT V-KAPPA: 4153-II[24].)
- SET 6: V19A'CL[87]. (IDENTICAL TO 1 RABBIT V-KAPPA: AH80-5[4].)

CDR3:
- SET 1: HK101'CL[5],HK134'CL[10]. (2 IDENTICAL)
- SET 2: LAY[39]. (IDENTICAL TO 1 HUMAN V-KAPPA-III: POM[48].)
- SET 3: Vb'CL[42],Vb''CL[43]. (2 IDENTICAL)

IDENTICAL SETS OF J-MINIGENES:
- SET 1: AU[2]. (IDENTICAL TO 1 HUMAN V-KAPPA-II: RPM1-6410'CL[16]; 2 HUMAN V-KAPPA-III: PIE[11],VKAPPA3'CL[82]; AND 1 HUMAN V-KAPPA-IV: PB17IV'CL[3].)
- SET 2: AG[7]. (IDENTICAL TO 1 HUMAN V-KAPPA-III: GOT[6].)
- SET 3: WALKER'CL[12]. (IDENTICAL TO 1 HUMAN V-KAPPA-II: TEW[1].)
- SET 4: DEN[46],BI[63]. (2 IDENTICAL HUMAN V-KAPPA-I; ALSO 1 HUMAN V-KAPPA-II: FR[14]; AND 3 HUMAN V-KAPPA-III: GAR'[10],FLO[12], IARC/BL41'CL[28].)

NOTES: HUMAN KAPPA LIGHT CHAINS SUBGROUP I (cont'd)

GENERAL NOTES:

SEE SIGNAL PEPTIDE TABLE IF # OCCURS AT POSITION 0.

SPECIFIC NOTES:

5) **HK101'CL:** THE SEQUENCE IS OBTAINED BY TRANSLATING THE NUCLEOTIDE SEQUENCE OF A CLONE OF HUMAN FOETAL LIVER DNA.

7) **AG:** THE AMINO ACID RESIDUES AT POSITIONS 39 AND 41 WERE REPORTED BY THE AUTHORS AS GLY AND LYS RESPECTIVELY; HOWEVER, THE PROOF WAS NOT ABSOLUTE. THUS, THEY ARE OMITTED.

9) **HK137'CL:** THE AMINO ACID SEQUENCE IS OBTAINED BY TRANSLATING THE NUCLEOTIDE SEQUENCE OF A CLONE OF HUMAN FETAL DNA.

10) **HK134'CL:** THE AMINO ACID SEQUENCE IS OBTAINED BY TRANSLATING THE NUCLEOTIDE SEQUENCE OF A CLONE OF HUMAN FETAL DNA.

17) **BJ26:** ACID RESIDUES AT POSITIONS 39 AND 41 OF BJ26 WERE REPORTED BY THE AUTHORS AS GLY AND LYS RESPECTIVELY. SINCE THIS PROTEIN WAS SEQUENCED BEFORE THE SEQUENCES OF MANY OTHER PROTEINS WERE KNOWN AT THESE TWO POSITIONS, WE HAVE OMITTED THEM.

33) **F-GUI:** THE SEQUENCES OF F-GUI AND S-GUI WERE FROM THE SAME PATIENT.

44) **HK102'CL:** THE SEQUENCE IS OBTAINED BY TRANSLATING THE NUCLEOTIDE SEQUENCE OF A CLONE OF HUMAN FOETAL LIVER DNA.

55) **S-GUI:** THE SEQUENCES OF F-GUI AND S-GUI WERE FROM THE SAME PATIENT.

56) **AMYLOID BAN:** AMINO ACID RESIDUES FOUND AT POSITIONS 104 AND 105 ARE VAL,LEU AND GLN,GLU RESPECTIVELY.

57) **BJ19:** THE AMINO ACID RESIDUES AT POSITIONS 39 AND 41 WERE REPORTED BY THE AUTHORS AS GLY AND LYS RESPECTIVELY. SINCE THIS PROTEIN WAS SEQUENCED BEFORE THE SEQUENCES OF MANY OTHER PROTEINS WERE KNOWN AT THESE TWO POSITIONS, WE HAVE OMITTED THEM.

59) **JBL:** THE AMINO ACID RESIDUE FOUND AT POSITION 34 WAS ALA OR SER.

64) **AMYLOID ES305:** THE AMINO ACID RESIDUES AT POSITIONS 21 AND 29 WERE ILE OR LEU.

74) **PW:** THE SEQUENCE WAS FROM A PATIENT WITH TRANSITIONAL CELL CARCINOMA OF THE URINARY BLADDER.

82) **RI:** THE SEQUENCE WAS FROM A PATIENT WITH TRANSITIONAL CELL CARCINOMA OF THE URINARY BLADDER.

109) **AMYLOID MS:** THE AMINO ACID RESIDUE AT POSITION 2 MS WAS ILE OR LEU.

111) **GM131'CL:** FROM AN EPSTEIN-BARR VIRUS-TRANSFORMED HUMAN LYMPHOID CELL LINE

+ THE FOLLOWING WERE EQUALLY AND MOST FREQUENTLY OCCURRING:

AT POSITION	RESIDUES
27C	(LEU,VAL)
27D	(TRP,GLU)
50	(ALA,ASP)
92	(TYR,ASP,ASN)
95A	(SER,GLY)
95B	(TRP,GLY)

HUMAN KAPPA LIGHT CHAINS SUBGROUP II

		INVARIANT RESIDUES	1 TEW	2 MIL	3 NIM	4 CUM	5 GM 607 'CL	6 BAT	7 BATES	8* ROB	9 SLO	10* WILS	11 GLI	12 AMYLOID TEW #	13 RAI	14* FR #	15 YOS	16 RPM1-6410 'CL #	17 MAN	18 KIR	19 HYL	20 MAG	21 TVE	22 EID	23 GAL (II)
	0		---	---	---	---	---	---	---	---	---	---	---	---	---	---	---	---	---	---	---	---	---	---	---
	1	ASP	ASP	ASP	ASP	ASP	ASP	ASP	ASP	ASP	ASP	ASP	ASP	ASP	ASP	ASP	ASP	ASP	---	ASP	---	---	---	---	---
	2	ILE(.97)	ILE	ILE	ILE	ILE	ILE	ILE	ILE	ILE	ILE	ILE	ILE	ILE	ILE	ILE	ILE	val		ILE	ILE	ILE	ILE	ILE	ASP
	3	VAL(.97)	VAL	VAL	VAL	VAL	VAL	VAL	VAL	VAL	VAL	VAL	VAL	VAL	VAL	VAL	VAL	VAL		VAL	VAL	VAL	VAL	VAL	ILE
	4		MET	MET	MET	MET	MET	MET	MET	MET	MET	MET	MET	MET	MET	MET	MET	MET		MET	MET	MET	MET	MET	VAL
	5	THR	THR	THR	THR	THR	THR	THR	THR	THR	THR	THR	THR	THR	THR	THR	THR	THR		THR	THR	THR	THR	THR	MET
	6	GLN	GLN	GLN	GLN	GLN	GLN	GLN	GLN	GLN	GLN	GLN	GLN	GLN	GLN	GLN	GLN	GLN		GLN	GLN	GLN	GLN	GLN	THR
	7	SER	SER	SER	SER	SER	SER	SER	SER	SER	SER	SER	SER	SER	SER	SER	SER	SER		SER	SER	SER	SER	SER	
	8	PRO	PRO	PRO	PRO	PRO	PRO	PRO	PRO	PRO	PRO	PRO	PRO	PRO	PRO	PRO	PRO	PRO		PRO	PRO	PRO	PRO	PRO	
	9	LEU	LEU	LEU	LEU	LEU	LEU	LEU	LEU	LEU	LEU	LEU	LEU	LEU	LEU	LEU	LEU	LEU	LEU	LEU	LEU	LEU	LEU	LEU	LEU
FR 1	10	SER	SER	SER	SER	SER	SER	SER	SER	SER	SER	SER	SER	SER	SER	SER	SER	SER	SER	SER	SER	SER	SER	SER	SER
	11	LEU	LEU	LEU	LEU	LEU	LEU	LEU	LEU	LEU	LEU	LEU	LEU	LEU	LEU	LEU	LEU	LEU	LEU	LEU	LEU	LEU	LEU	LEU	LEU
	12	PRO(.96)	PRO	PRO	PRO	PRO	PRO	PRO	PRO	PRO	PRO	PRO	PRO	PRO	PRO	PRO	PRO	PRO	PRO	PRO	PRO	PRO	PRO	PRO	PRO
	13	VAL(.96)	VAL	VAL	VAL	VAL	VAL	VAL	VAL	VAL	VAL	VAL	VAL	VAL	VAL	VAL	gly	VAL	VAL	VAL	VAL	VAL	VAL	VAL	VAL
	14	THR	THR	THR	THR	THR	THR	THR	THR	THR	THR	THR	THR	THR	THR	THR	THR	THR							
	15		PRO	PRO	PRO	PRO	PRO	PRO	PRO	PRO	PRO	PRO	PRO	PRO	PRO	PRO	PRO	leu							
	16	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY							
	17		GLU	GLU	GLU	GLU	GLU	GLU	GLU	GLU	GLU	GLU	GLU	GLU	GLU	GLU	GLU	gln							
	18	PRO	PRO	PRO	PRO	PRO	PRO	PRO	PRO	PRO	PRO	PRO	PRO	PRO	PRO	PRO	PRO	PRO							
	19	ALA	ALA	ALA	ALA	ALA	ALA	ALA	ALA	ALA	ALA	ALA	ALA	ALA	ALA	ALA	ALA	ALA							
	20	SER	SER	SER	SER	SER	SER	SER	SER	SER	SER	SER	SER	SER	SER	SER	SER	SER							
	21	ILE	ILE	ILE	ILE	ILE	ILE	ILE	ILE	ILE	ILE	ILE	ILE	ILE	ILE	ILE	ILE	ILE							
	22		SER	SER	SER	SER	SER	SER	SER	SER	SER	SER	SER	SER	ILE	SER	SER	SER							
	23	CYS	CYS	CYS	CYS	CYS	CYS	CYS	CYS	CYS	CYS	CYS	CYS	CYS	CYS	CYS	CYS	CYS							
	24	ARG	ARG	ARG	ARG	ARG	ARG	ARG	ARG	ARG	ARG	ARG	ARG		ARG	ARG		ARG	ARG						ARG
	25		SER	SER	SER	SER	SER	SER	SER	ALA	SER	SER	SER			SER		SER							
	26	SER	SER	SER	SER	SER	SER	SER	SER	SER	SER	SER	SER	SER		SER		SER							
	27		GLN	GLN	GLN	GLN	GLN	GLN	GLN	GLX	GLN	GLN	GLN	SER		GLN		GLN							
	27A		SER	ASN	SER	SER	SER	SER		ARG	SER	SER	SER	GLX		SER		SER							
	27B	LEU	LEU	LEU	LEU	LEU	LEU	LEU	LEU	---	LEU	LEU	LEU			LEU		LEU							
CDR 1	27C		LEU	LEU	LEU	LEU	LEU	LEU	LEU	---	ARG	LEU	LEU			VAL		VAL							
	27D		HIS	GLX	TRP	ASP	HIS	HIS		---	HIS					TYR		TYR							
	27E		SER	---	SER	SER	SER	SER		---						ARG		SER							
	27F		---	---		GLY	---	---	---	---	ASX					---		---							
	28		ASP	SER	ASP	ASP	ASN	ASX	ASX	VAL						ASX		ASP							
	29		GLY	ASX	GLY	GLY	GLY	GLY	GLY	LEU						GLY		GLY							
	30		PHE	GLY	TYR	ASN	TYR	ASX	ASX							ASX		ASN							
	31		ASP	ASX	LYS	THR	ASN	ASX	ASX							THR		THR							
	32	TYR	TYR	TYR	TYR	TYR	TYR	TYR	TYR							TYR		TYR							
	33	LEU	LEU	LEU	LEU	LEU	LEU	LEU								LEU		LEU							
	34		ASN	ASP	ASN	ASN	ASP	ASX								ASX		ASN							
	35	TRP	TRP	TRP	TRP	TRP	TRP	TRP								TRP		TRP							
	36		TYR	TYR	TYR	TYR	TYR	TYR								TYR		PHE							
	37		LEU	LEU	LEU	LEU	LEU	LEU								LEU		GLN							
	38		GLN	GLX	GLN	GLN	GLN	GLX								GLN		GLN							
	39		LYS	LYS	LYS	LYS	LYS	LYS																	
	40		PRO	PRO	PRO	ALA	PRO	PRO								LYS		ARG							
FR 2	41	GLY	GLY	GLY	GLY	GLY	GLY	GLY								PRO		PRO							
	42		GLN	GLX	GLN	GLN	GLN	GLX								GLY		GLY							
	43	SER		SER	SER	SER	SER									GLN		GLN							
	44	PRO		PRO	PRO	PRO	PRO	PRO								SER		SER							
	45			GLX	GLN	GLN	GLN	GLX								PRO		PRO							
	46		LEU	LEU	LEU	LEU	LEU									GLU		ARG							
	47	LEU	LEU	LEU	LEU	LEU	LEU									LEU		ARG							
	48	ILE	ILE	ILE	ILE	ILE	ILE									LEU		LEU							
	49	TYR		TYR	TYR	TYR	TYR									ILE		ILE							
	50			LEU	LEU	THR	LEU									TYR		TYR							
	51			GLY	GLY	LEU	GLY									LEU		LYS							
CDR 2	52	SER	SER	SER	SER	SER	SER									SER		VAL							
	53		ASN	ASN	ASN	TYR	ASN									SER		SER							
	54	ARG	ARG	ARG	ARG	ARG	ARG									TYR		ASN							
	55		ALA	ALA	ALA	ALA	ALA									ARG		ARG							
	56	SER	SER	SER	SER	SER	SER									ASP		ASP							
	57	GLY	GLY	GLY	GLY	GLY	GLY									SER		SER							
	58	VAL	VAL	VAL	VAL	VAL	VAL									GLY		GLY							
	59	PRO	PRO	PRO	PRO	PRO	PRO									VAL		VAL							
	60		ASP	ASN	ASP	ASP	ASP									PRO		PRO							
	61	ARG	ARG	ARG	ARG	ARG	ARG									ASP		ASP							
	62	PHE	PHE	PHE	PHE	PHE	PHE									ARG		ARG							
	63	SER	SER	SER	SER	SER	SER								PHE	PHE		PHE							
	64		GLY	GLY	GLY	GLY	GLY								SER	SER		SER							
	65	SER	SER	SER	SER	SER	SER								GLY	ASP		GLY							
	66	GLY	GLY	GLY	GLY	GLY	GLY								SER	SER		SER							
	67	SER	SER	SER	SER	SER	SER								GLY	GLY		GLY							
	68		GLY	GLY	ASP	GLY	GLY								SER	SER		SER							
	69	THR	THR	THR	THR	THR	THR								GLY	GLY		GLY							
	70		ASP	ASX	ASP	ASP	ASP									THR		THR							
FR 3	71	PHE	PHE	PHE	PHE	PHE	PHE									ASP		ASP							
	72	THR	THR	THR	THR	THR	THR								PHE	PHE		PHE							
	73	LEU	LEU	LEU	LEU	LEU	LEU								THR	THR		THR							
	74		LYS	LYS	ILE	LYS	LYS								LEU	LEU		LEU							
	75	ILE	ILE	ILE	ILE	ILE	ILE								ASX	LYS		LYS							
	76		SER	SER	SER	SER	SER								ILE	ILE		ILE							
	77	ARG	ARG	ARG	ARG	ARG	ARG								SER	THR		SER							
	78	VAL	VAL	VAL	VAL	VAL	VAL								ARG	ARG		ARG							
	79		GLU	GLX	GLU	GLN	GLU									VAL		VAL	VAL						
	80		ALA	ALA	PRO	ALA	ALA									GLN		GLU	GLX						
	81		GLU	GLX	GLU	GLU	GLU									ALA		ALA	ALA						
	82		ASP	ASX	ASP	ASP	ASP									GLU		GLU	GLX						
	83	VAL	VAL	VAL	VAL	VAL	VAL									ASP		ASP	ASX						
	84	GLY	GLY	GLY	GLY	GLY	GLY									VAL		VAL	VAL						
	85	VAL	VAL	VAL	VAL	VAL	VAL									GLY		GLY	GLY						
	86	TYR	TYR	TYR	TYR	TYR	TYR									VAL		VAL	VAL						
	87	TYR	TYR	TYR	TYR	TYR	TYR									TYR		TYR	TYR						
	88	CYS	CYS	CYS	CYS	CYS	CYS									TYR		TYR	TYR						
	89	MET	MET	MET	MET	MET	MET									CYS		CYS	CYS						
	90		GLX	GLN	GLN	GLN	ALA									MET		MET							
	91		ALA	ALA	ALA	ARG	ALA									GLN		GLN							
	92		LEU	LEU	LEU	LEU	LEU									ALA		GLY							
	93		GLN	GLN	GLN	GLU	GLN									THR		THR							
	94		ALA	THR	SER	ILE	THR									GLX		HIS							
CDR 3	95		PRO	PRO	PRO	PRO	PRO									SER		TRP							
	95A		---	---	---	---										PRO		SER							
	95B		---	---	---	---	---									---		---							
	95C		---	---	---	---	---									---		---							
	95D		---	---	---	---	---									---		---							
	95E		---	---	---	---	---									---		---							
	95F		---	---	---	---	---									---		---							
	96		ILE	LEU	PRO	TYR	GLN									---		---							
	97	THR	THR	THR	THR	THR	THR									TYR		TRP							
	98	PHE	PHE	PHE	PHE	PHE	PHE									THR		THR							
	99	GLY	GLY	GLY	GLY	GLY	GLY									PHE		PHE							
	100		GLN	GLY	GLN	GLN	GLN									GLY		GLY							
	101	GLY	GLY	GLY	GLY	GLY	GLY									GLN		GLN							
	102	THR	THR	THR	THR	THR	THR									GLY		GLY							
	103		ARG	ASN	LYS	LYS	LYS									THR		THR							
FR 4	104		LEU	VAL	LEU	LEU	VAL									LYS		LYS							
	105		GLU	GLU	GLU	GLU	GLU									LEU		VAL	VAL						
	106	ILE	ILE	ILE	ILE	ILE	ILE									GLX		GLU	GLU						
	106A		---	---	---	---	---									ILE		ILE	ILE						
	107		LYS	LYS	LYS	ARG	LYS									---		---							
	108	ARG	ARG	ARG	ARG	ARG	ARG									LYS		LYS	LYS						
	109	THR		THR	THR	THR										ARG		ARG							
																THR									

HUMAN KAPPA LIGHT CHAINS SUBGROUP II (cont'd)

		24* GIL	25 MEH	26 SC	27* TH	28 SYV	29 LUT	30 ROB 2	31 RAI 2	# OF SEQUENCES	# OF AMINO ACIDS	OCCURRENCES OF MOST COMMON AMINO ACID	VARIABILITY
	0	---	---	---	---	---	---	---	---	31	1	31(ASP)	1.
	1	ASP	ASP	ASP	ASP	ASP	ASP	ASP	ASP	30	2	29(ILE)	2.1
	2	ILE	ILE	ILE	ILE	ILE	ILE	ILE	ILE	30	2	29(VAL)	2.1
	3	VAL	VAL	VAL	VAL	VAL	VAL	VAL	met	30	3	28(MET)	3.2
	4	MET	MET	MET	MET	MET	MET	leu	thr				
	5	THR	THR	THR	THR	THR	THR			28	1	28(THR)	1.
	6	GLN	GLN	GLN	GLN	GLN	GLN			27	1	27(GLN)	1.
	7	SER	SER	GLN	SER					25	1	25(SER)	1.
	8	PRO	PRO	SER	PRO					24	1	24(PRO)	1.
	9	LEU	LEU							25	1	25(LEU)	1.
	10	SER								24	1	24(SER)	1.
FR	11	LEU								24	1	24(LEU)	1.
1	12	ser								24	2	23(PRO)	2.1
	13									23	2	22(VAL)	2.1
	14									17	1	17(THR)	1.
	15									17	2	16(PRO)	2.1
	16									17	1	17(GLY)	1.
	17									17	2	16(GLU)	2.1
	18									17	1	17(PRO)	1.
	19									17	1	17(ALA)	1.
	20									17	1	17(SER)	1.
	21									17	1	17(ILE)	1.
	22									17	2	16(SER)	2.1
	23									17	1	17(CYS)	1.
	24									16	1	16(ARG)	1.
	25									14	2	13(SER)	2.2
	26									14	1	14(SER)	1.
	27									14	1 : 2	14(GLN) : 12(GLN)	1. : 2.3
	27A									12	3	10(SER)	
	27B									12	1	12(LEU)	
	27C									12	3	9(LEU)	
CDR	27D									10	5	5(HIS)	
	27E									7	2	6(SER)	
1	27F									2	2	1(+)	
	28									10	4	7(ASP) : 4(+)	5.7 : 10.
	29									10	3	8(GLY)	3.8
	30									9	4 : 5	5(ASN) : 3(ASP)	7.2 : 15.
	31									9	4	4(ASN) : 3(+)	9. : 12.
	32									9	1	9(TYR)	1.
	33									8	1	8(LEU)	1.
	34									8	2	6(ASN) : 4(+)	2.7 : 4.
	35									8	1	8(TRP)	1.
	36									8	2	7(TYR)	2.3
	37									8	2	7(LEU)	2.3
	38									8	1 : 2	8(GLN) : 6(GLN)	1. : 2.7
	39									8	2	7(LYS)	2.3
	40									8	2	7(PRO)	2.3
FR	41									8	1	8(GLY)	1.
2	42									8	1 : 2	8(GLN) : 6(GLN)	1. : 2.7
	43									6	1	6(SER)	1.
	44									7	1	7(PRO)	1.
	45									7	3	5(GLN) : 3(+)	4.2 : 7.
	46									7	2	6(LEU)	2.3
	47									7	1	7(LEU)	1.
	48									7	1	7(ILE)	1.
	49									6	1	6(TYR)	1.
	50									6	3	4(LEU)	4.5
	51									6	4	3(GLY)	8.
CDR	52									7	1	7(SER)	1.
	53									7	2	5(ASN)	2.8
2	54									7	1	7(ARG)	1.
	55									7	2	5(ALA)	2.8
	56									7	1	7(SER)	1.
	57									7	1	7(GLY)	1.
	58									7	1	7(VAL)	1.
	59									7	1	7(PRO)	1.
	60									7	2	6(ASP)	2.3
	61									7	1	7(ARG)	1.
	62									8	1	8(PHE)	1.
	63									8	1	8(SER)	1.
	64									8	2	7(GLY)	2.3
	65									8	1	8(SER)	1.
	66									8	1	8(GLY)	1.
	67									8	1	8(SER)	1.
	68									8	2	7(GLY)	2.3
	69									7	1	7(THR)	1.
	70									7	1 : 2	7(ASP) : 6(ASP)	1. : 2.3
FR	71									8	1	8(PHE)	1.
	72									8	1	8(THR)	1.
3	73									8	1	8(LEU)	1.
	74									8	3	6(LYS)	4.
	75									8	1	8(ILE)	1.
	76									8	2	7(SER)	2.3
	77									8	1	8(ARG)	1.
	78									8	1	8(VAL)	1.
	79									8	2	6(GLU) : 4(+)	2.7 : 4.
	80									8	2	7(ALA)	2.3
	81									8	1 : 2	8(GLU) : 6(GLU)	1. : 2.7
	82									8	1 : 2	8(ASP) : 6(ASP)	1. : 2.7
	83									8	1	8(VAL)	1.
	84									8	1	8(GLY)	1.
	85									8	1	8(VAL)	1.
	86									8	1	8(TYR)	1.
	87									8	1	8(TYR)	1.
	88									8	1	8(CYS)	1.
	89									7	1	7(MET)	1.
	90									7	1 : 2	7(GLN) : 6(GLN)	1. : 2.3
	91									7	3	5(ALA)	4.2
	92									7	2	5(LEU)	2.8
	93									7	3	5(GLN) : 4(GLN)	4.2 : 5.3
	94									7	5	2(+)	18.
CDR	95									7	2	6(PRO)	2.3
3	95A												
	95B												
	95C												
	95D												
	95E												
	95F												
	96									7	6	2(TYR)	21.
	97									7	1	7(THR)	1.
	98									7	1	7(PHE)	1.
	99									7	1	7(GLY)	1.
	100									7	2	6(GLN)	2.3
	101									7	1	7(GLY)	1.
FR	102									7	1	7(THR)	1.
4	103									7	3	5(LYS)	4.2
	104									8	2	4(+)	4.
	105									8	1 : 2	8(GLU) : 7(GLU)	1. : 2.3
	106									8	1	8(ILE)	1.
	106A												
	107									8	2	7(LYS)	2.3
	108									7	1	7(ARG)	1.
	109									4	1	4(THR)	1.

ANTIBODY SPECIFICITIES: HUMAN KAPPA LIGHT CHAINS SUBGROUP II

8) **ROB:** COLD AGGLUTININ WITH ANTI-PR1D ACTIVITY
10) **WILS:** COLD AGGLUTININ WITH ANTI-BLOOD GROUP I ACTIVITY
14) **FR:** ANTI-PHOSPHOCHOLINE(BINDING CONSTANT=6.4X10EXP4)
24) **GIL:** ANTI-IGG
27) **TH:** COLD AGGLUTININ WITH ANTI-PR2 ACTIVITY (RBC MEMBRANE ANTIGEN ON HUMAN, RAT AND GUINEA PIG ERYTHROCYTES INACTIVATED BY PROTEOLYTIC ENZYMES AND NEURAMINIDASE)

REFERENCE: HUMAN KAPPA LIGHT CHAINS SUBGROUP II

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2) **MIL:** DREYER,W.J.,GRAY,W.R. & HOOD,L. (1967) COLD SPRING HARBOR SYMP. QUANTITATIVE BIOL.,32,353-367.
3) **NIM:** EULITZ,M. & KLEY,H.-P. (1977) IMMUNOCHEM.,14,289-297. (CHECKED BY AUTHOR 10/18/77)
4) **CUM:** HILSCHMANN,N. & CRAIG,L.C. (1965) PROC.NAT.ACAD.SCI.USA,53,1403-1409; HILSCHMANN,N. (1967) Z.PHYSIOL.CHEM.,348,1718-1722; HILSCHMANN,N. (1969) NATURE,,56,195-205. (CHECKED BY AUTHOR)
5) **GM 607'CL:** KLOBECK,H.G.,SOLOMON,A. & ZACHAU,H.G. (1984) NATURE,309,73-76.
6) **BAT:** DAYHOFF,M.O. (1972) ATLAS OF PROTEIN SEQUENCE & STRUCTURE,5,D-246. SUBMITTED BY SMITHIES,O.,GIBSON,D.M. AND FANNING,E.M. (CHECKED BY AUTHOR)
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8) **ROB:** GERGELY,J.,WANG,A.C. & FUDENBERG,H.H. (1973) VOX SANG.,24,432-440. (CHECKED BY AUTHOR)
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11) **GLI:** FRANGIONE,B.,FRANKLIN,E.C. & PRELLI,F. (1976) SCAND.J.IMMUNOL.,5,623-627. (CHECKED BY AUTHOR 10/17/77)
12) **AMYLOID TEW:** TERRY,W.D.,PAGE,D.L.,KIMURA,S.,ISOBE,T.,OSSERMAN,E.F. & GLENNER,G.G. (1973) J.CLIN.INVEST.,52,1276-1281. (CHECKED BY AUTHOR 03/02/84)
13) **RAI:** MILSTEIN,C.P. & MILSTEIN,C. (1971) BIOCHEM.J.,121,211-215. (CHECKED BY AUTHOR WHO PROVIDED ADDITIONAL RESIDUES TO THOSE PUBLISHED)
14) **FR:** RIESEN,W.,RUDIKOFF,S.,ORIOL,R. & POTTER,M. (1975) BIOCHEMISTRY,14,1052-1057; RIESEN,W.F.,BRAUN,D.G. & JATON,J.C. (1976) PROC.NAT.ACAD.SCI.USA,73,2096-2100; RIESEN,W.F. & JATON,J.C. (1976) BIOCHEMISTRY,15,3829-3833. (CHECKED BY AUTHOR 12/05/77)
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16) **RPM1-6410'CL:** HIETER,P.A.,MAX,E.E.,SEIDMAN,J.G.,MAIZEL,J.V.,JR. & LEDER,P. (1980) CELL,22,197-207; KLOBECK,H.G,MEINDL,A.,COMBRIATO,G., SOLOMON,A. & ZACHAU,H.G. (1985) NUC.ACIDS RES.,13,6499-6513.
17) **MAN:** MILSTEIN,C. (1969) PROC. 5TH FEBS SYMP.,15,43-56. (CHECKED BY AUTHOR WHO PROVIDED ADDITIONAL RESIDUES TO THOSE PUBLISHED)
18) **KIR:** SLETTEN,K.,HANNESTAD,K. & HARBOE,M. (1974) SCAND.J.IMMUNOL.,3,215-218. (CHECKED BY AUTHOR 12/05/77)
19) **HYL:** SLETTEN,K.,HANNESTAD,K. & HARBOE,M. (1974) SCAND.J.IMMUNOL.,3,215-218. (CHECKED BY AUTHOR 12/05/77)
20) **MAG:** SLETTEN,K.,HANNESTAD,K. & HARBOE,M. (1974) SCAND.J.IMMUNOL.,3,215-218. (CHECKED BY AUTHOR 12/05/77)
21) **TVE:** SLETTEN,K.,HANNESTAD,K. & HARBOE,M. (1974) SCAND.J.IMMUNOL.,3,215-218. (CHECKED BY AUTHOR 12/05/77)
22) **EID:** SLETTEN,K.,HANNESTAD,K. & HARBOE,M. (1974) SCAND.J.IMMUNOL.,3,215-218. (CHECKED BY AUTHOR 12/05/77)
23) **GAL(II):** MILSTEIN,C.,JARVIS,J.M. & MILSTEIN,C.P. (1969) J.MOL.BIOL.,46,599-602. (CHECKED BY AUTHOR)
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25) **MEH:** SLETTEN,K.,HANNESTAD,K. & HARBOE,M. (1974) SCAND.J.IMMUNOL.,3,215-218. (CHECKED BY AUTHOR 12/05/77)
26) **SC:** SEON,B.K.,YAGI,Y. & PRESSMAN,D. (1973) J.IMMUNOL.,110,345-349. (CHECKED BY AUTHOR)
27) **TH:** GERGELY,J.,WANG,A.C. & FUDENBERG,H.H. (1973) VOX SANG.,24,432-440. (CHECKED BY AUTHOR)
28) **SYV:** SLETTEN,K.,HANNESTAD,K. & HARBOE,M. (1974) SCAND.J.IMMUNOL.,3,215-218. (CHECKED BY AUTHOR 12/05/77)
29) **LUT:** SLETTEN,K.,HANNESTAD,K. & HARBOE,M. (1974) SCAND.J.IMMUNOL.,3,215-218. (CHECKED BY AUTHOR 12/05/77)
30) **ROB2:** MOULIN,A. & FOUGEREAU,M. (1973) NATURE NEW BIOLOGY,246,176-178.
31) **RAI2:** MOULIN,A. & FOUGEREAU,M. (1973) NATURE NEW BIOLOGY,246,176-178.

NOTES: HUMAN KAPPA LIGHT CHAINS SUBGROUP II

IDENTICAL SETS OF FRAMEWORK SEGMENTS:

FR1: SET 1: TEW[1],MIL[2],NIM[3],CUM[4],GM 607 'CL[5],BAT[6],BATES[7],ROB[8],SLO[9],WILS[10],GLI[11],AMYLOID TEW[12],RAI[13]. (13 IDENTICAL)

FR2: SET 1: MIL[2],NIM[3],GM 607 'CL[5]. (3 IDENTICAL HUMAN V-KAPPA-II; ALSO 2 MOUSE V-KAPPA-II: VKAPPA 24B'CL[63],2S1.3[67].)
SET 2: MIL[2],FR[14]. (2 IDENTICAL)

FR3: SET 1: TEW[1],GM 607 'CL[5],RPM1-6410'CL[16]. (3 IDENTICAL)

FR4: SET 1: GM 607 'CL[5],RPM1-6410'CL[16]. (2 IDENTICAL HUMAN V-KAPPA-II; ALSO 3 HUMAN V-KAPPA-I: AU[2],GAL(I)[36],CL'[110]; 7 HUMAN V-KAPPA-III: WOL[2],PAY[7],PIE[11],GLO[15],CUR[20],REE[57],VKAPPA3'CL[82]; AND 1 HUMAN V-KAPPA-IV: PB17IV'CL[3].)
SET 2: NIM[3],FR[14]. (2 IDENTICAL HUMAN V-KAPPA-II; ALSO 3 HUMAN V-KAPPA-I: AG[7],DEN[46],BI[63]; 6 HUMAN V-KAPPA-III: NEU[5], GOT[6],GAR'[10],FLO[12],FR4[21],IARC/BL41'CL[28]; AND 1 HUMAN V-KAPPA-IV: LEN[4].)
SET 3: TEW[1]. (IDENTICAL TO 2 HUMAN V-KAPPA-I: WALKER'CL[12],OU(IOC)[34].)

IDENTICAL SETS OF COMPLEMENTARITY DETERMINING REGIONS:

CDR1:

CDR2: SET 1: MIL[2],NIM[3],GM 607 'CL[5]. (3 IDENTICAL)

CDR3:

IDENTICAL SETS OF J-MINIGENES:

SET 1: RPM1-6410'CL[16]. (IDENTICAL TO 1 HUMAN V-KAPPA-I: AU[2]; 2 HUMAN V-KAPPA-III: PIE[11],VKAPPA3'CL[82]; AND 1 HUMAN V-KAPPA-IV: PB17IV'CL[3].)
SET 2: TEW[1]. (IDENTICAL TO 1 HUMAN V-KAPPA-I: WALKER'CL[12].)
SET 3: FR[14]. (IDENTICAL TO 2 HUMAN V-KAPPA-I: DEN[46],BI[63]; AND 3 HUMAN V-KAPPA-III: GAR'[10],FLO[12],IARC/BL41'CL[28].)

SPECIFIC NOTES:

12) **AMYLOID TEW:** IT HAS THE SAME SEQUENCE AS THAT OF TEW SO FAR AS THE SEQUENCED POSITIONS ARE CONCERNED.
14) **FR:** AN IDIOTYPIC ANTIBODY TO FR NOT INHIBITABLE BY PHOSPHORYLCHOLINE REACTED BETTER WITH THE FR HEAVY CHAIN THAN WITH THE LIGHT CHAIN. THE CROSS-REACTION WITH MOPC167 WAS 10,000 TIMES WEAKER. (RIESEN,W.F. (1979) EUR.J.IMMUNOL.,9,421-425.)
16) **RPM1-6410'CL:** THE AMINO ACID SEQUENCE IS OBTAINED BY TRANSLATING THE NUCLEOTIDE SEQUENCE OF A CLONE OF HUMAN ADULT DNA.

+ THE FOLLOWING WERE EQUALLY AND MOST FREQUENTLY OCCURRING:

AT POSITION	RESIDUES
27F	(GLY,ASN) : (GLY,ASP)
28	(ASP,ASN)
31	(THR,ASP)
34	(ASP,ASN)
45	(GLU,GLN)
79	(GLU,GLN)
94	(THR,SER)
104	(LEU,VAL)

HUMAN KAPPA LIGHT CHAINS SUBGROUP III

		INVARIANT RESIDUES	1 TI	2* WOL	3* SIE	4 NG9 CL #	5* NEU	6* GOT	7* PAY	8* SON	9* WEI	10 GAR	11* PIE	12* FLO	13* LOP	14* SCA	15* GLO	16 SAL	17 WIL	18* MA	19* NIC	20* CUR	21 FR4	22* DRE	23* PER	24 CAM
	0		---	---	---	---	---	---	---	---	---	---	---	---	---	---	---	---	---	---	---	---	GLX	GLU	GLU	---
	1		GLU	GLU	GLU	GLU	GLU	GLU	GLU	GLU	GLU	GLU	GLU	GLU	GLU	GLU	GLU	GLU	GLU	GLU	GLU	GLU	ILE	ILE	ILE	GLU
	2		ILE	ILE	ILE	ILE	ILE	ILE	ILE	ILE	ILE	ILE	ILE	ILE	ILE	ILE	ILE	VAL	VAL	VAL	VAL	VAL	VAL	VAL	VAL	ILE
	3	VAL(.96)	VAL	VAL	VAL	VAL	VAL	VAL	VAL	VAL	VAL	VAL	VAL	VAL	VAL	VAL	LEU	LEU	LEU	LEU	LEU	LEU	LEU	LEU	LEU	VAL
	4		LEU	LEU	LEU	LEU	LEU	LEU	LEU	LEU	LEU	LEU	LEU	LEU	LEU	LEU										LEU
	5	THR	THR	THR	THR	THR	THR	THR	THR	THR	THR	THR	THR	THR	THR	THR	THR	THR	THR	THR	THR	THR	THR	THR	THR	THR
	6		GLN	GLN	GLN	GLN	GLN	GLN	GLN	GLN	GLN	GLN	GLN	GLN	GLN	GLN	GLN	GLN	GLN	GLN	GLN	GLN	GLN	GLX	GLX	GLN
	7	SER	SER	SER	SER	SER	SER	SER	SER	SER	SER	SER	SER	SER	SER	SER	SER	SER	SER	SER	SER	SER	SER	SER	SER	SER
	8	PRO	PRO	PRO	PRO	PRO	PRO	PRO	PRO	PRO	PRO	PRO	PRO	PRO	PRO	PRO	PRO	PRO	PRO	PRO	PRO	PRO	PRO	PRO	PRO	PRO
	9		GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY
FR1	10		THR	THR	THR	THR	THR	THR	THR	THR	THR	THR	THR	THR	THR	THR	THR	THR	THR	THR	THR	THR	THR	THR	THR	THR
	11	LEU(.99)	LEU	LEU	LEU	LEU	LEU	LEU	LEU	LEU	LEU	LEU	LEU	LEU	LEU	LEU	LEU	LEU	LEU	LEU	LEU	LEU	LEU	LEU	LEU	LEU
	12	SER	SER	SER	SER	SER	SER	SER	SER	SER	SER	SER	SER	SER	SER	SER	SER	SER	SER	SER	SER	SER	SER	SER	SER	SER
	13		LEU	LEU	LEU	LEU	LEU	LEU	LEU	LEU	LEU	LEU	LEU	LEU	LEU	LEU	LEU	LEU	LEU	LEU	LEU	LEU	LEU	LEU	LEU	LEU
	14	SER(.97)	SER	SER	SER	SER	SER	SER	SER	SER	SER	SER	SER	SER	SER	SER	SER	SER	SER	SER	SER	SER	SER	SER	SER	SER
	15	PRO(.98)	PRO	PRO	PRO	PRO	PRO	PRO	PRO	PRO	PRO	PRO	PRO	PRO	PRO	PRO	PRO	PRO	PRO	PRO	PRO	PRO	PRO	PRO	PRO	PRO
	16	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLX	GLY
	17		GLU	GLU	GLU	GLU	GLU	GLU	GLU	GLU	GLU	GLU	GLU	GLU	GLU	GLU	GLU	GLU	GLU	GLU	GLU	GLU	GLU	GLX	GLX	GLU
	18		ARG	ARG	ARG	ARG	ARG	ARG	ARG	ARG	ARG	ARG	ARG	ARG	ARG	ARG	ARG	ARG	ARG	ARG	ARG	ARG	ARG	ARG	ARG	ARG
	19		ALA	ALA	ALA	ALA	ALA	ALA	ALA	ALA	ALA	ALA	ALA	ALA	ALA	ALA	ALA	ALA	ALA	ALA	ALA	ALA	ALA	ALA	ALA	ALA
	20		THR	THR	THR	THR	THR	THR	THR	THR	THR	THR	THR	THR	THR	THR	THR	THR	THR	THR	THR	THR	THR	THR	THR	THR
	21	LEU(.95)	LEU	LEU	LEU	LEU	LEU	LEU	LEU	LEU	LEU	LEU	LEU	LEU	LEU	LEU	LEU	LEU	LEU	LEU	LEU	LEU	LEU	LEU	LEU	LEU
	22	SER(.97)	SER	SER	SER	SER	SER	SER	SER	SER	SER	SER	SER	SER	SER	SER	SER	SER	SER	SER	SER	SER	SER	SER	SER	
	23	CYS	CYS	CYS	CYS	CYS	CYS	CYS	CYS	CYS	CYS	CYS	CYS	CYS	CYS	CYS	CYS	CYS	CYS	CYS	CYS	CYS	CYS	CYS	CYS	
	24		ARG	ARG	ARG	ARG	ARG	ARG	ARG	ARG	ARG	ARG	ARG	ARG	ARG	ARG	ARG	ARG	ARG	ARG	ARG	ARG	ARG	ARG	ARG	ARG
	25	ALA(.98)	ALA	ALA	ALA	ALA	ALA	ALA	ALA	ALA	ALA	ALA	SER	ALA	ALA	ALA	SER	GLY	ALA	ALA	ALA	ALA	ALA	ALA	ALA	ALA
	26		SER	SER	SER	SER	SER	SER	SER	SER	SER	SER	SER	SER	SER	SER	SER	GLY	SER	SER	SER	SER	SER	SER	SER	SER
	27		GLN	GLN	GLN	GLN	GLN	GLN	GLN	GLN	GLN	GLN	GLN	GLN	GLN	GLN	GLN	GLN	GLN	GLN	GLN	GLN	GLN	GLX	GLN	GLN
	27A		SER	SER	SER	SER	SER	SER	SER	SER	SER	SER	SER	SER	SER	GLY	SER	SER	SER	SER	SER	SER	SER			SER
	27B		---	---	---	---	---	---	---	---	---	---	---	---	---	---	---	---	---	---	---	---	---	---	---	---
CDR1	27C		---	---	---	---	---	---	---	---	---	---	---	---	---	---	---	---	---	---	---	---	---	---	---	---
	27D		---	---	---	---	---	---	---	---	---	---	---	---	---	---	---	---	---	---	---	---	---	---	---	---
	27E		---	---	---	---	---	---	---	---	---	---	---	---	---	---	---	---	---	---	---	---	---	---	---	---
	27F		---	---	---	---	---	---	---	---	---	---	---	---	---	---	---	---	---	---	---	---	---	---	---	---
	28		VAL	VAL	VAL	VAL	VAL	VAL	VAL	VAL	VAL	VAL	VAL	VAL	VAL	ILE	VAL	SER	VAL	VAL	VAL	VAL	VAL	VAL		VAL
	29		SER	SER	SER	SER	SER	ARG	SER	SER	SER	SER	SER	SER	SER	SER	SER	VAL	SER	SER	SER	SER	ARG	SER		SER
	30		ASN	SER	ASN	SER	SER	SER	SER	SER	SER	SER	SER	SER	SER	ASN	SER	SER	ASN			SER	ASN	SER		SER
	31		SER	GLY	SER	SER	ARG	SER	SER	SER	SER	SER	TYR	TYR	TYR	TYR	TYR	TYR	MET			TYR	TYR	TYR		TYR
	32		PHE	TYR	TYR	TYR	TYR	TYR	TYR	TYR	TYR	TYR	LEU	LEU	LEU	LEU	LEU	VAL	LEU			LEU	LEU	LEU		LEU
	33		LEU	LEU	LEU	LEU	LEU	LEU	LEU	LEU	LEU	LEU														
	34		ALA	GLY	ALA	ALA	ALA	ALA	ALA	ALA	ALA	ALA	ALA	ALA	ALA	ALA	ALA	ALA	ALA			ALA	ALA	ALA		ALA
	35	TRP	TRP	TRP	TRP	TRP	TRP	TRP	TRP	TRP	TRP	TRP	TRP	TRP	TRP	TRP		TRP	TRP	TRP		TRP	TRP	TRP		TRP
	36	TYR	TYR	TYR	TYR	TYR	TYR	TYR	TYR	TYR	TYR	TYR	TYR	TYR	TYR	TYR	TYR	TYR	TYR	TYR		TYR	TYR			TYR
	37		GLN	GLN	GLN	GLN	GLN	GLN	GLN	GLN	GLN	GLN	GLN	GLN	GLN	GLN	GLN	GLN	GLN	GLN		GLN	GLN			GLN
	38		GLN	GLN	GLN	GLN	GLN	GLN	GLN	GLN	GLN	GLN	GLN	GLN	GLN	GLN	GLN	GLN				GLN	GLN			GLN
	39		LYS	LYS	LYS	LYS	LYS	LYS	ARG	LYS	LYS	LYS	LYS	LYS	LYS	LYS		LYS	LYS			LYS	ARG			
	40		PRO	PRO	PRO	PRO	PRO	PRO	PRO	PRO	PRO	PRO	PRO	PRO	PRO	PRO	PRO	PRO	PRO			PRO	PRO			
FR2	41	GLY(.96)	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY				GLY	GLY			
	42		GLN	GLN	GLN	GLN	GLN	GLN	GLN	GLN	GLN	GLN	GLN	GLN	GLN	GLN	GLN	GLN				GLN	GLN			
	43		ALA	ALA	ALA	ALA	ALA	ALA	ALA	ALA	ALA	ALA	ALA	ALA	ALA	ALA		ALA				ALA	ALA			
	44		PRO	PRO	PRO	PRO	PRO	PRO	PRO	PRO	PRO	PRO	PRO	PRO	PRO	PRO		PRO				PRO	PRO			
	45		ARG	ARG	ARG	ARG	ARG	ARG	ARG	ARG	ARG	ARG	ARG	ARG	ARG	ARG		ARG				ARG	LYS			
	46	LEU(.96)	LEU	LEU	LEU	LEU	LEU	LEU	LEU	LEU	LEU	LEU	LEU	LEU	LEU			LEU				LEU				
	47	LEU(.96)	LEU	LEU	LEU	LEU	LEU	LEU	LEU	LEU	LEU	LEU	LEU	LEU	LEU			LEU				LEU				
	48		ILE	ILE	ILE	ILE	ILE	ILE	ILE	ILE	ILE	ILE	ILE	ILE	ILE			ILE				ILE				
	49		TYR	TYR	TYR	TYR	TYR	TYR	TYR	TYR		TYR	TYR	TYR				TYR				TYR				
	50		VAL	GLY	GLY	GLY	GLY	GLY	GLY	GLY		GLY	GLY	GLY				GLY				GLY				
	51		ALA	ALA	ALA	ALA	ALA	ALA	ALA	ALA		ALA	ALA	ALA				ALA				ALA				
	52		SER	SER	SER	THR	SER	SER	SER	SER		SER	SER	SER				SER				SER				
	53		SER	SER	SER	SER	SER	SER	SER	SER		SER	SER	SER				SER				SER				
CDR2	54	ARG(.95)	ARG	ARG	ARG	ARG	ARG	ARG	ARG	ARG		ARG	ARG	ARG				ARG				ARG				
	55		ALA	ALA	ALA	ALA	ALA	ALA	ALA	ALA		ALA	ALA	ALA				ALA				ALA	ALA			
	56		THR	THR	THR	THR	THR	THR	THR	THR		THR	THR	THR				THR				THR	THR			
	57	GLY(.96)	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY		GLY	GLY	GLY				GLY				GLY	GLY			
	58		ILE	ILE	ILE	ILE	ILE	ILE	ILE	ILE		ILE	ILE	ILE				ILE				ILE	ILE			
	59	PRO	PRO	PRO	PRO	PRO	PRO	PRO	PRO	PRO		PRO	PRO	PRO				PRO				PRO	PRO			
	60		ASP	ASP	ASP	ASP	ASP	ASP	ASP	ASN		ASP	ASP	ASP				ASP				ASP	ASP			
	61	ARG	ARG	ARG	ARG	ARG	ARG	ARG	ARG	ARG		ARG	ARG	ARG				ARG				ARG	ARG			
	62	PHE	PHE	PHE	PHE	PHE	PHE	PHE	PHE	PHE		PHE	PHE	PHE				PHE				PHE	PHE			
	63		SER	SER	SER	SER	THR	SER	SER	SER		SER	SER	SER				SER				SER	SER			
	64	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY		GLY	GLY	GLY				GLY				GLY	GLY			
	65	SER(.95)	SER	SER	SER	SER	SER	SER	SER	SER		SER	SER	SER				SER				SER	SER			
	66		GLY	GLY	GLY	ALA	GLY	GLY	GLY	GLY		GLY	GLY	GLY				GLY				GLY	GLY			
	67	SER(.95)	SER	SER	SER	SER	SER	SER	SER	SER		SER	SER	SER				SER				SER	SER			
	68	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY		GLY	GLY	GLY				GLY				GLY	GLY			
	69	THR(.95)	THR	THR	THR	THR	THR	THR	THR	THR		THR	THR	THR				THR				THR	THR			
	70		ASP	ASP	ASP	ASP	ASP	ASP	ASP	ASP		ASP	ASP	ASP				ASP				ASP	ASP			
	71	PHE	PHE	PHE	PHE	PHE	PHE	PHE	PHE	PHE		PHE	PHE	PHE				PHE				PHE	PHE			
FR3	72	THR	THR	THR	THR	THR	THR	THR	THR	THR		THR	THR	THR				THR				THR	THR			
	73	LEU	LEU	LEU	LEU	LEU	LEU	LEU	LEU	LEU		LEU	LEU	LEU				LEU				LEU	LEU			
	74	THR(.95)	THR	THR	THR	THR	THR	THR	THR	THR		THR	THR	THR				THR				THR	THR			
	75	ILE(.95)	ILE	ILE	ILE	ILE	VAL	ILE	ILE	ILE		ILE	ILE	ILE				ILE				ILE	ILE			
	76		SER	SER	SER	SER	SER	SER	SER	SER		SER	SER	SER				SER				SER	SER			
	77		GLY	GLY	GLY	ARG	ARG	ARG	ARG	ARG		ARG	ARG	ARG				ARG				ARG	ARG			
	78		LEU	LEU	LEU	LEU	LEU	LEU	LEU	LEU		LEU	LEU	LEU				LEU				LEU	LEU			
	79		GLU	GLU	GLU	GLU	GLU	GLU	GLU	GLU		GLU	GLU	GLU				GLU				GLU	GLU			
	80		PRO	PRO	PRO	PRO	PRO	PRO	PRO	PRO		PRO	PRO	PRO				PRO				PRO	PRO			
	81	GLU(.95)	GLU	GLU	ASP	GLU	GLU	GLU	GLU	GLU		GLU	GLU	GLU				GLU				GLU	GLU			
	82	ASP	ASP	ASP	ASP	ASP	ASP	ASP	ASP	ASP		ASP	ASP	ASP				ASP				ASP	ASP			
	83		PHE	PHE	PHE	PHE	PHE	PHE	PHE	PHE		PHE	PHE	PHE				PHE				PHE	PHE			
	84	ALA	ALA	ALA	ALA	ALA	ALA	ALA	ALA	ALA		ALA	ALA	ALA				ALA				ALA	ALA			
	85	VAL(.95)	VAL	VAL	VAL	VAL	VAL	VAL	VAL	VAL		VAL	VAL	VAL				VAL				VAL	VAL			
	86	TYR	TYR	TYR	TYR	TYR	TYR	TYR	TYR	TYR		TYR	TYR	TYR				TYR				TYR	TYR			
	87		TYR	TYR	TYR	TYR	TYR	TYR	TYR	TYR		TYR	TYR	TYR				TYR				TYR	PHE			
	88	CYS	CYS	CYS	CYS	CYS	CYS	CYS	CYS	CYS		CYS	CYS	CYS				CYS				CYS	CYS			
	89	GLN(.95)	GLN	GLN	GLN	GLN	GLN	GLN	GLN	GLN		GLN	GLN	GLN				GLN				GLN	GLN			
	90	GLN	GLN	GLN	GLN	GLN	GLN	GLN	GLN	GLN		GLN	GLN	GLN				GLN				GLN	GLN			
	91		TYR	TYR	TYR	TYR	TYR	TYR	TYR	TYR		TYR	TYR	TYR				TYR				TYR	TYR			
	92		GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY		GLY	GLY	GLY				GLY				GLY	GLY			
	93		SER	SER	SER	ASN	ALA	SER	SER	SER		SER	SER	SER				SER				SER	GLY			
	94		SER	LEU	SER	SER	SER	SER	SER	SER		SER	SER	SER				SER				SER	PRO			
CDR3	95		PRO	GLY	PRO	GLN	PRO	PRO	PRO	PRO		PRO	PRO	PRO				PRO				---	---			
	95A		---	---	---	---	---	---	---	---		---	---	---				---				---	---			
	95B		---	---	---	---	---	---	---	---		---	---	---				---				---	---			
	95C		---	---	---	---	---	---	---	---		---	---	---				---				---	---			
	95D		---	---	---	---	---	---	---	---		---	---	---				---				---	---			
	95E		---	---	---	---	---	---	---	---		---	---	---				---				---	---			
	95F		---	---	---	---	---	---	---	---		---	---	---				---				---	---			
	96		SER	ARG	GLN	---	CYS	ARG	LEU	TYR		TYR	TRP	TYR				LEU				ARG	GLN			
	97	THR(.95)	THR	THR	THR	---	THR	THR	THR	THR		THR	THR	THR				THR				THR	PRO			
	98	PHE	PHE	PHE	PHE	---	PHE	PHE	PHE	PHE		PHE	PHE	PHE				PHE				PHE	PHE			
	99	GLY	GLY	GLY	GLY	---	GLY	GLY	GLY	GLY		GLY	GLY	GLY				GLY				GLY	GLY			
	100		GLN	GLN	GLN	---	GLN	GLN	GLN	GLY		GLN	GLN	GLN				GLN				GLN	GLN			
	101	GLY	GLY	GLY	GLY	---	GLY	GLY	GLY	GLY		GLY	GLY	GLY				GLY				GLY	GLY			
	102		THR	THR	SER	---	THR	THR	THR	THR		THR	THR	THR				THR				THR	THR			
FR4	103		LYS	LYS	LYS	---	LYS	LYS	LYS	LYS		LYS	LYS	LYS				LYS				LYS	LYS			
	104		VAL	VAL	VAL	---	LEU	LEU	VAL	VAL		LEU	VAL	LEU				VAL				VAL	LEU			
	105		GLU	GLU	GLU	---	GLU	GLU	GLU	GLU		GLU	GLU	GLU				GLU				GLU	GLU			
	106		LEU	ILE	ILE	---	ILE	ILE	ILE	ILE		ILE	ILE	ILE				ILE				ILE	ILE			
	106A		---	---	---	---	---	---	---	---		---	---	---				---				---	---			
	107	LYS(.95)	LYS	LYS	LYS	---	LYS	LYS	LYS	LYS		LYS	LYS	LYS				LYS				LYS	LYS			
	108	ARG	ARG	ARG	ARG	---	ARG	ARG	ARG	ARG		ARG	ARG	ARG				ARG				ARG				
	109	THR	THR				THR	THR	THR	THR		THR	THR	THR				THR				THR				

HUMAN KAPPA LIGHT CHAINS SUBGROUP III (cont'd)

		25* STE	26* GJ	27* TAK	28 IARC/ BL41 CL	29 RAD	30 DIL	31 CAS	32 MCE' #	33 KEA	34 SMI	35* AJ	36 BRO 'IGG	37 NIG	38 IKE	39 TIL	40 AMYLOID KSA	41 POL	42* CLA #	43* SHE' #	44 JH #	45 WIN	46 LEA	47 ARP	48* POM	49 VAND
	0	---	---	---	---	---	---	---	---	---	---	---	---	---	---	---	---	---	---	---	---	---	---	---	---	---
	1	GLU	GLU	GLU	GLU	GLU	GLU	GLU	GLU	GLU	GLU	GLU	GLU	lys	GLU	GLU	GLU	GLU	GLU	GLU	asp	lys	GLU	GLU	GLU	GLU
	2	ILE	ILE	ILE	ILE	ILE	ILE	ILE	ILE	ILE	ILE	ILE	ILE	ILE	ILE	ILE	ILE	ILE	ILE	ILE	ILE	ILE	phe	ILE	ILE	ILE
	3	VAL	VAL	VAL	VAL	VAL	VAL	VAL	VAL	VAL	VAL	VAL	VAL	VAL	VAL	VAL	VAL	VAL	VAL	VAL	VAL	VAL	VAL	VAL	VAL	VAL
	4	LEU	LEU	LEU	LEU	LEU	LEU	LEU	LEU	LEU	LEU	LEU	LEU	LEU	LEU	LEU	met	LEU	met	met	met	LEU	LEU	LEU	met	met
	5	THR	THR	THR	THR	THR	THR	THR	THR	THR	THR	THR	THR	THR	THR	THR	THR	THR	THR	THR	THR	THR	THR	THR	THR	THR
	6	GLN	GLN	GLX	GLN	GLN	GLN	GLN	GLN	GLN	GLN	GLN	glu	GLN	GLN	GLN	GLN	glu	GLN	GLN	GLN	GLN	GLX	GLN	GLN	GLN
	7	SER	SER	SER	SER	SER	SER	SER	SER	SER	SER	SER	SER	SER	SER	SER	SER	SER	SER	SER	SER	SER	SER	SER	SER	SER
	8	PRO	PRO	PRO	PRO	PRO	PRO	PRO	PRO	PRO	PRO	PRO	PRO	PRO	PRO	PRO	PRO	PRO	PRO	PRO	PRO	PRO	PRO	PRO	PRO	PRO
	9	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	ala	ala	asp	GLY	GLY	pro	ala	GLY	ala	#	#	#	ala	ala	GLY	val	ala
FR1	10	THR	THR	THR	THR	THR	THR	THR	THR	THR	THR	THR	THR	THR	THR	THR	THR	THR	THR	THR	THR	THR	THR	THR	THR	THR
	11	LEU	LEU	LEU	LEU	LEU	LEU	LEU	LEU	LEU	LEU	LEU	LEU	LEU	LEU	LEU	LEU	LEU	LEU	LEU	LEU	LEU	LEU	LEU	LEU	LEU
	12	SER	SER	SER	SER	SER	SER	SER	SER	SER	SER	SER	SER	SER	SER	SER	SER	SER	SER	SER	SER	SER	SER	SER	SER	SER
	13	LEU	LEU	LEU	LEU	LEU	LEU	LEU	phe	LEU	LEU	LEU	LEU	LEU	LEU	LEU	val	LEU	val	val	SER	LEU	LEU	val	val	SER
	14	SER	SER	SER	SER	SER	SER	SER	SER	SER	SER	SER	SER	SER	SER	SER	SER	SER	SER	SER	SER	SER	SER	SER	SER	SER
	15	PRO	PRO	PRO	PRO	PRO	PRO	PRO	PRO	PRO	PRO	PRO	PRO	PRO	PRO	PRO	PRO	PRO	PRO	PRO	PRO	PRO	PRO	PRO	PRO	PRO
	16	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY
	17	GLU	GLU	GLX	GLU	asp	asp	asp	GLU	GLU	GLU	GLU	GLU	GLU	GLU	GLU	GLU	GLX	GLU	GLU	GLU	GLX	GLU	GLU	GLU	GLU
	18	ARG	ARG	ARG	ser	ARG	ARG	ARG	ARG	ARG	ARG	ARG	ARG	ARG	ARG	ARG	ARG	ARG	ARG	ARG	ARG	ARG		ARG	ARG	ARG
	19	ALA	val	val	ALA	ALA	ALA	ALA	ALA	ALA	ALA	ALA	ALA	ALA	ALA	val	ALA	ALA	ALA	ALA	ALA	ALA	ALA	ALA	ALA	ALA
	20	ala	THR	THR	THR	THR	THR	THR	THR	THR	THR	THR	THR	THR	ala	THR	THR	THR	THR	THR	THR	THR	ile	THR	THR	THR
	21	LEU	LEU	LEU	LEU	LEU	LEU	LEU	LEU	LEU	LEU	LEU	LEU	LEU	LEU	LEU	LEU	LEU	LEU	LEU	LEU	LEU	LEU	LEU	LEU	LEU
	22	SER	SER	SER	SER	SER	SER	SER	SER	SER	SER	SER	SER	SER	SER	SER	SER	SER	SER	SER	SER	SER	SER	SER	SER	SER
	23		CYS	CYS	CYS	CYS	CYS		CYS	CYS		CYS			CYS	CYS	CYS	CYS	CYS				CYS	CYS	CYS	CYS
	24		ARG	ARG	ARG	ARG	ARG		ARG	ARG		ARG	ARG		ARG	ARG	ARG	ARG	ARG		THR		ARG	ARG	ARG	ARG
	25		ALA	ALA	ALA	ALA	ALA		ALA	ALA		ALA	ALA		ALA	ALA	ALA	ALA	ALA		ALA		ALA	ALA	ALA	ALA
	26		SER	SER	SER	SER	SER		SER	GLY		SER	SER		SER	SER	SER	SER	SER				SER	SER	SER	SER
	27			GLX	GLN	GLN	GLN		GLN	SER		GLN	GLN		GLN	GLN	GLX	GLX					GLX	GLN	GLN	GLN
	27A			SER	---	VAL	SER		---	---		SER	SER		SER	---	THR	---					---	---	SER	---
	27B			---	---	---	---		---	---		---	---		---	---	---	---					---	---	---	---
CDR1	27C			---	---	---	---		---	---		---	---		---	---	---	---					---	---	---	---
	27D			---	---	---	---		---	---		---	---		---	---	---	---					---	---	---	---
	27E			---	---	---	---		---	---		---	---		---	---	---	---					---	---	---	---
	27F			---	---	---	---		---	---		---	---		---	---	---	---					---	---	---	---
	28			VAL	SER	SER	LEU		SER	ASX		VAL	VAL		VAL	SER	LEU	SER					SER	HIS	ILE	ASX
	29			SER	VAL	SER	ASX			VAL		SER	ARG		SER	VAL		VAL					VAL	VAL	SER	ILE
	30				SER	ASN	SER			ALA			SER		ASN	SER		ARG					SER	ILE	ASN	GLY
	31			SER	SER	SER	LYS			LYS			SER		SER	SER							LEU	ALA	SER	SER
	32			TYR	ASN	TYR	SER			SER			TYR		TYR	TYR		TYR					TYR	GLY	TYR	ASN
	33			LEU	LEU	LEU	LEU			LEU			LEU		LEU	LEU		LEU					LEU	TYR	LEU	LEU
	34			ALA	ALA	ALA	SER			ALA			ASP		ALA	ALA		ALA					ALA	ALA	ALA	ALA
	35				TRP	TRP	TRP			TRP			TRP		TRP	TRP								TRP	TRP	TRP
	36				TYR	TYR	TYR			TYR			TYR		TYR	TYR	TYR							TYR	TYR	TYR
	37				GLN	GLN	GLX			GLX			GLN		GLN	GLN	GLN							GLN	GLN	GLX
	38				GLN	GLN	GLX			GLX			GLN		GLN									GLN	GLN	GLX
	39				LYS	LYS	LYS			LYS			LYS		ARG		SER							LYS	LYS	LYS
	40				ARG	PRO	PRO			PRO			PRO		PRO		PRO							PRO	PRO	PRO
FR2	41				GLY	GLY	GLY										GLY								SER	GLY
	42				GLN	GLN	GLX										GLN								GLY	ARG
	43				SER	ALA	THR										ALA								SER	ALA
	44				PRO	PRO	PRO										PRO								PRO	PRO
	45				ARG	ARG	ARG										ARG								ARG	ARG
	46				LEU		LEU										LEU								LEU	LEU
	47				LEU		LEU										LEU								LEU	
	48				ILE		ILE										ILE								ILE	
	49				ARG		TYR										TYR								TYR	
	50				ASP												GLY								GLY	
	51				ALA												THR								ALA	
	52				SER												SER								SER	
	53				SER												THR								THR	
CDR2	54				ARG												ARG								ARG	
	55				ALA	ALA											ALA								ALA	
	56				ASN	THR											THR								THR	
	57				GLY	GLY											GLY								GLY	
	58				ILE	THR											ILE								ILE	
	59				PRO	PRO											PRO								PRO	
	60				ASP	VAL											ALA								ALA	
	61				ARG	ARG											ARG								ARG	
	62				PHE	PHE											PHE								PHE	
	63				SER	SER											SER								SER	
	64				GLY	GLY											GLY								GLY	
	65				SER	SER																			SER	
	66				GLY	GLU																			GLY	
	67				SER	SER																			SER	
	68				GLY	GLY																			GLY	
	69				THR	THR																			THR	
	70				ASP	ASP																			GLU	
	71				PHE	PHE																			PHE	
FR3	72				THR	THR																			THR	
	73				LEU	LEU																			LEU	
	74				ILE	THR																			THR	
	75				ILE	ILE																			ILE	
	76				SER	SER																			SER	
	77				ARG	ARG																			SER	
	78				LEU	LEU																			LEU	
	79				GLU	GLU																			GLN	
	80				PRO	PRO																			SER	
	81				GLU	GLU																			GLU	
	82				ASP	ASP																			ASP	
	83				PHE	PHE																			PHE	
	84				ALA	ALA																			ALA	
	85				VAL	VAL																			VAL	
	86				TYR	TYR																			TYR	
	87				TYR	TYR																			TYR	
	88				CYS	CYS																			CYS	
	89				GLN	GLN																			GLN	
	90				GLN	GLN																			GLN	
	91				TYR	TYR																			TYR	
	92				SER	GLU																			ASN	
	93				THR	THR																			ASN	
	94				SER	SER																			TRP	
	95				PRO	PRO																			PRO	
CDR3	95A				---	---																			---	
	95B				---	---																			---	
	95C				---	---																			---	
	95D				---	---																			---	
	95E				---	---																			---	
	95F				---	---																			---	
	96				TYR	THR																			PRO	
	97				THR	THR																			THR	
	98				PHE	PHE																			PHE	
	99				GLY	GLY																			GLY	
	100				GLN	GLN																			GLN	
	101				GLY	GLY																			GLY	
	102				THR	THR																			THR	
FR4	103				LYS	ARG																			ARG	
	104				LEU	LEU																			VAL	
	105				GLU	ASP																			GLU	
	106				ILE	ILE																			ILE	
	106A				---	---																			---	
	107				LYS	LYS																			LYS	
	108				ARG																				ARG	
	109																									

HUMAN KAPPA LIGHT CHAINS SUBGROUP III (cont'd)

		50 AMYLOID SO124	51 DOV	52 SHM	53 GRA	54* GOE II	55 LOW*	56 VER	57 REE	58 WE #	59 HOW	60 HS4	61 HBJ 5	62* TEH	63* CRA (III)	64* PLA	65* PIN	66 MCE	67 HAC	68 K-EV15 CL	69 BER	70* BOR	71* DRI	72* WAL	73* GOL	74* GAG
	0	---	---	---	---	---	---	---	---	---	---	---	---	---	---	---	---	---	---	---	---	---	---	---	---	---
	1	GLU	GLU	GLU	GLU	asp	GLU	GLU	GLU	asp	GLU	GLU	GLU	GLU	GLU	GLU	GLU	GLU	GLU	GLU	GLU	GLU	GLU	GLU	GLU	GLU
	2	ILE	ILE	ILE	met	ILE	ILE	thr	leu	ILE	ILE	VAL	VAL	VAL	VAL	VAL	VAL	VAL	VAL	thr	ILE	ILE	ILE	ILE	ILE	VAL
	3	VAL	VAL	VAL	VAL	VAL	VAL	VAL	VAL	gln	LEU	LEU	LEU	LEU	LEU	LEU	LEU	LEU	LEU	LEU	VAL	VAL	VAL	VAL	VAL	LEU
	4	met	met	met	met	LEU	met	LEU	LEU	met											LEU	LEU	LEU	LEU	LEU	
	5	THR	THR	THR	THR	THR	THR	THR	THR	THR	THR	THR	THR	THR	THR	THR	THR	THR	THR	THR	THR	THR	THR	THR	THR	THR
	6	GLN	GLN	GLN	GLN	GLN	GLN	GLN	GLN	GLN	GLN	GLN	GLN	GLN	GLN	GLN	GLN	GLN	GLN	GLN	GLX	GLX	GLN	GLN	GLN	GLN
	7	SER	SER	SER	SER	SER	SER	SER	SER	SER	SER	SER	SER	SER	SER	SER	SER	SER	SER	SER	SER	SER	SER	SER	SER	SER
	8	PRO	PRO	PRO	PRO	PRO	PRO	PRO	PRO	PRO	PRO	PRO	PRO	PRO	PRO	PRO	PRO	PRO	PRO	PRO	PRO	PRO	PRO	PRO	PRO	
	9	ala	ala	ala	ala	ala	ala	GLY	ala	ser	GLY	GLY	asx	GLY	GLY	GLY	GLY	GLY	GLY	ala	GLY	ala				
FR1	10	THR	THR	THR	THR	ser	gly	THR	THR	ser	THR	THR	THR	THR	THR	THR	THR			phe	THR	THR				
	11	LEU	LEU	LEU	LEU	LEU	LEU	LEU	LEU	LEU	LEU	LEU	LEU	LEU	LEU	LEU	LEU			met						
	12	SER	SER	SER	SER	SER	SER	SER	LEU	SER	SER	SER	SER	LEU	LEU	LEU	LEU			SER						
	13	val	val	val	met	val	val	LEU	val	ala	LEU	LEU	LEU	LEU	LEU	LEU	LEU			ala						
	14	SER	SER	SER	SER	thr	SER	SER	SER	SER	SER	SER	SER	SER	SER	SER	SER			thr						
	15	PRO	PRO	PRO	PRO	PRO	PRO	PRO	PRO	val	PRO	PRO	PRO	PRO	PRO	PRO	PRO			PRO						
	16	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY							GLY						
	17	GLU	GLU	GLU	GLU	GLU	gly	GLU	GLU	asp	GLU	GLU	GLX							asp						
	18	ARG	ser	gly	ARG	ARG	thr	val	glu											lys						
	19	val	ALA	ALA	ALA	ALA	ALA	val	val	val										val						
	20	THR	THR	THR	THR	ser	THR	THR	THR	#										asn						
	21	LEU	LEU	LEU	LEU	LEU	LEU	ile	LEU	ile										ile						
	22	SER	SER	SER	SER	SER	SER	tyr	SER	thr										SER						
	23	CYS	CYS	CYS		CYS	CYS	CYS	CYS											CYS						
	24	ARG	ARG	ARG			SER	LYS	ARG											LYS						
	25	ALA	ALA	ALA			ALA	SER	ALA	ALA										ALA						
	26		SER	SER			GLY		SER	SER										SER						
	27		GLU	GLU			GLN		GLU	GLN										GLN						
	27A		---	---			---	---	---	---										---						
	27B		---	---			---	---	---	---										---						
CDR1	27C		---	---			---	---	---	---										---						
	27D		---	---			---	---	---	---										---						
	27E		---	---			---	---	---	---										---						
	27F		---	---			---	---	---	---										---						
	28		SER	THR			SER	LEU	SER	THR										ASP						
	29		VAL	VAL			VAL	SER	LEU	#										ILE						
	30		SER	ALA			ASP		SER	GLY										ASP						
	31		THR	LYS			GLX		ASP											ASP						
	32		ASX	SER			THR		ASN											ASP						
	33		LEU	LEU			VAL	LEU	VAL	#										MET						
	34		ALA	ALA			ALA	ALA	ALA											ASN						
	35		TRP	TRP			TRP	TRP	TRP											TRP						
	36		TYR	TYR			TYR	TYR	TYR											TYR						
	37		GLX	GLX			GLX	GLN	GLN											GLN						
	38		GLX	GLX			GLX	GLN	HIS											GLN						
	39		LYS				LYS		LYS											LYS						
	40		PRO				PRO		PRO											PRO						
FR2	41								GLY											GLY						
	42								GLN											GLU						
	43								ALA											ALA						
	44							LEU	PRO											ALA						
	45							ARG	ARG											ILE						
	46							LEU	LEU											PHE						
	47							LEU	LEU											ILE						
	48							ILE	LEU											ILE						
	49							TYR	TYR											GLN						
	50							GLY	ALA											GLU						
	51							VAL	THR											ALA						
CDR2	52							SER	SER											THR						
	53							THR	THR											THR						
	54							ARG	ARG											LEU						
	55							ALA	PRO											VAL						
	56							ALA	THR											PRO						
	57							GLY	ASP											GLY						
	58							ILE	ILE											ILE						
	59							PRO	PRO											PRO						
	60							ASP	ALA											PRO						
	61							ARG	ARG											ARG						
	62							PHE	PHE											PHE						
	63							THR	SER											SER						
	64							GLY	GLY											GLY						
	65							ARG	SER											SER						
	66							ALA	MET											GLY						
	67							SER	SER											TYR						
	68							GLY	GLY											GLY						
	69							THR	THR											THR						
	70							ASP	GLU											ASP						
FR3	71							PHE	PHE											PHE						
	72							THR	THR											THR						
	73							LEU	LEU											LEU						
	74							THR	THR											THR						
	75							ILE	ILE											ILE						
	76							SER	PHE											ASN						
	77							ASP	ARG											ASN						
	78							LEU	VAL											ILE						
	79							GLU	GLU											GLU						
	80							PRO	SER											SER						
	81							GLU	GLU											GLU						
	82							ASP	ASP											ASP						
	83							PHE	SER											ALA						
	84							ALA	ALA											ALA						
	85							VAL	VAL											TYR						
	86							TYR	TYR											TYR						
	87							TYR	TYR											PHE						
	88							CYS	CYS											CYS						
	89							GLN	GLN											LEU						
	90							GLN	GLN											GLN						
	91							TYR	HIS											HIS						
	92							ASP	GLU											ASP						
	93							THR	---											ASN						
	94							SER	---											PHE						
	95							PRO	---											PRO						
CDR3	95A							---	---											---						
	95B							---	---											---						
	95C							---	---											---						
	95D							---	---											---						
	95E							---	---											---						
	95F							---	---											---						
	96							LEU	---											---						
	97							THR	THR											---						
	98							PHE	PHE											---						
	99							GLY	GLY											---						
	100							GLY	GLN											---						
	101							GLY	GLY											---						
	102							THR	THR											---						
FR4	103							LYS	LYS											---						
	104							LEU	VAL											---						
	105							ASP	GLU											---						
	106							VAL	ILE											---						
	106A							---	---											---						
	107							ARG	LYS											---						
	108								ARG											---						
	109																			---						

HUMAN KAPPA LIGHT CHAINS SUBGROUP III (cont'd)

		75 DOB	76 HS6	77 HBJ 12	78 BUR (K)	79 LEG	80 B6	81 AMYLOID WR #	82 VKAPPA3 CL #	# OF SEQUENCES	# OF AMINO ACIDS	OCCURRENCES OF MOST COMMON AMINO ACID	VARIABILITY
	0	---	---	---	---	---							
	1	GLU	GLU	GLU	GLU	GLU				79	3 : 4	74(GLU) : 73(GLU)	3.2 : 4.3
	2	ILE	ILE	ILE	ILE	ILE				79	5	74(ILE)	5.3
	3	ile	VAL	VAL	VAL	VAL				79	4	76(VAL)	4.2
	4	met	LEU	val	LEU	LEU				79	3	65(LEU)	3.6
	5	THR	THR	THR						77	1	77(THR)	1.
	6	GLN	GLN	GLN						77	2	75(GLN) : 69(GLN)	2.1 : 2.2
	7	SER								75	1	75(SER)	1.
	8	PRO								74	1	74(PRO)	1.
	9	ala								69	6 : 7	46(GLY)	9. : 11.
	10									70	4	66(THR)	4.2
FR1	11									68	2	67(LEU)	2.
	12									67	1	67(SER)	1.
	13									67	5	52(LEU)	6.4
	14									66	2	64(SER)	2.1
	15									66	2	65(PRO)	2.
	16									62	1	62(GLY)	1.
	17									62	3 : 4	56(GLU) : 50(GLU)	3.3 : 5.
	18						ARG			58	7	51(ARG)	8.
	19						ALA			60	2	52(ALA)	2.3
	20						ala			59	5	53(THR)	5.6
	21						LEU			60	2	57(LEU)	2.1
	22						SER			60	3	58(SER)	3.1
	23						CYS			50	1	50(CYS)	1.
	24						ARG			51	4	47(ARG)	4.3
	25						ALA			52	2	51(ALA)	2.
	26						SER			49	2	46(SER)	2.1
	27						GLN			47	3	43(GLN) : 37(GLN)	3.3 : 3.8
	27A						SER			32	4	29(SER)	
	27B						---						
	27C						---						
CDR1	27D						---						
	27E						---						
	27F						---						
	28						LEU			47	7 : 8	25(VAL)	13. : 15.
	29						SER			44	6	27(SER)	9.8
	30						GLY			40	7	24(SER)	12.
	31						ASN			39	10	24(SER)	16.
	32						TYR			40	8	28(TYR)	11.
	33						LEU			41	4	36(LEU)	4.6
	34						ALA			41	5	37(ALA)	5.5
	35						TRP	TRP		38	1	38(TRP)	1.
	36						TYR	TYR		39	1	39(TYR)	1.
	37						GLN	GLN		39	1 : 2	39(GLN) : 33(GLN)	1. : 2.4
	38						GLN	GLN		37	2 : 3	36(GLN) : 30(GLN)	2.1 : 3.7
	39						LYS	LYS		33	3	29(LYS)	3.4
	40						PRO	PHE		34	3	32(PRO)	3.2
FR2	41						GLY	GLY		27	2	26(GLY)	2.1
	42						GLN	GLN		27	4	24(GLN) : 23(GLN)	4.5 : 4.7
	43						ALA	ALA		26	3	23(ALA)	3.4
	44						PRO	PRO		27	3	25(PRO)	3.2
	45						ARG			26	3	24(ARG)	3.3
	46						LEU	LEU		24	2	23(LEU)	2.1
	47						LEU	LEU		23	2	22(LEU)	2.1
	48						MET	ILE		22	3	20(ILE)	3.3
	49						TYR	PHE		22	4	19(TYR)	4.6
	50						GLY	ASP		21	5	16(GLY)	6.6
	51						VAL			20	3	16(ALA)	3.8
CDR2	52						SER			20	2	18(SER)	2.2
	53						SER	SER		21	2	16(SER)	2.6
	54						ARG	#		20	2	19(ARG)	2.1
	55						ALA	ALA		23	3	21(ALA)	3.3
	56						THR			22	4	19(THR)	4.6
	57						GLY	GLY		23	2	22(GLY)	2.1
	58						ILE	VAL		23	3	21(ILE)	3.3
	59						PRO		PRO	23	1	23(PRO)	1.
	60						ASP		ASP	23	5	17(ASP)	6.8
	61						ARG		ARG	23	1	23(ARG)	1.
	62						PHE		PHE	23	1	23(PHE)	1.
	63						SER		SER	23	2	21(SER)	2.2
	64						GLY		GLY	23	1	23(GLY)	1.
	65						SER		SER	22	2	21(SER)	2.1
	66						GLY		ALA	22	4	17(GLY)	5.2
	67						SER		SER	22	2	21(SER)	2.1
	68						GLY		GLY	22	1	22(GLY)	1.
	69						ALA		THR	22	2	21(THR)	2.1
	70								ASP	21	2	19(ASP)	2.2
	71								PHE	21	1	21(PHE)	1.
FR3	72								THR	21	1	21(THR)	1.
	73								LEU	21	1	21(LEU)	1.
	74								THR	21	2	20(THR)	2.1
	75								ILE	21	2	20(ILE)	2.1
	76								SER	21	3	19(SER)	3.3
	77						ARG		ARG	22	5	16(ARG)	6.9
	78						LEU		LEU	22	3	20(LEU)	3.3
	79						GLX		GLU	22	2	21(GLU) : 20(GLU)	2.1 : 2.2
	80						PRO		PRO	22	2	19(PRO)	2.3
	81						GLU		GLU	22	2	21(GLU)	2.1
	82						ASP		ASP	22	1	22(ASP)	1.
	83						PHE		PHE	22	3	20(PHE)	3.3
	84						ALA		ALA	22	1	22(ALA)	1.
	85						VAL		VAL	22	2	21(VAL)	2.1
	86						TYR		TYR	22	1	22(TYR)	1.
	87						TYR		TYR	22	2	20(TYR)	2.2
	88						CYS		CYS	22	1	22(CYS)	1.
	89						GLN		GLN	22	2	21(GLN)	2.1
	90						GLN		GLN	22	1	22(GLN)	1.
	91						TYR		TYR	22	2	20(TYR)	2.2
	92						GLY		GLY	22	5	16(GLY)	6.9
	93						SER		ASN	21	5	12(SER)	8.8
	94						SER		SER	21	4	18(SER)	4.7
	95						PRO		GLN	21	3	18(PRO)	3.5
CDR3	95A						---		---	1	1	1(PRO)	
	95B						---		---				
	95C						---		---				
	95D						---		---				
	95E						---		---				
	95F						---		---				
	96						PHE		TRP	19	10	4(TYR)	48.
	97						THR		THR	20	2	19(THR)	2.1
	98						PHE		PHE	20	1	20(PHE)	1.
	99						GLY		GLY	20	1	20(GLY)	1.
	100						GLN		GLN	20	2	18(GLN)	2.2
	101						GLY		GLY	20	1	20(GLY)	1.
	102						SER		THR	20	2	18(THR)	2.2
	103						LYS		LYS	20	2	18(LYS)	2.2
FR4	104						LEU		VAL	20	2	11(VAL)	3.6
	105						GLU		GLU	20	2	18(GLU)	2.2
	106						ILE		ILE	20	3	18(ILE)	3.3
	106A						---		---				
	107						LYS		LYS	20	2	19(LYS)	2.1
	108								ARG	16	1	16(ARG)	1.
	109									10	1	10(THR)	1.

ANTIBODY SPECIFICITIES: HUMAN KAPPA LIGHT CHAINS SUBGROUP III

2) **WOL:** ANTI-HUMAN GAMMA G GLOBULIN; WA IDIOTYPE
3) **SIE:** ANTI-HUMAN GAMMA G GLOBULIN; WA IDIOTYPE
5) **NEU:** CRYOGLOBULIN WITH ANTI-IGG ACTIVITY; B IDIOTYPE (KUNKEL,H.G.,WINCHESTER,R.J.,JOSLIN,F.G. & CAPRA,J.D. (1974) J.EXP.MED.,139,128)
6) **GOT:** CRYOGLOBULIN WITH ANTI-IGG ACTIVITY; B IDIOTYPE
7) **PAY:** CRYOGLOBULIN WITH ANTI-IGG ACTIVITY; B IDIOTYPE
8) **SON:** CRYOGLOBULIN WITH ANTI-LOW-DENSITY LIPOPROTEIN ACTIVITY; B IDIOTYPE
9) **WEI':** CRYOGLOBULIN WITH ANTI-LOW-DENSITY LIPOPROTEIN ACTIVITY; B IDIOTYPE
10) **GAR':** CRYOGLOBULIN WITH ANTI-IGG ACTIVITY; B IDIOTYPE
11) **PIE:** AUTOANTIBODY WHICH BINDS SPECIFICALLY TO INTERMEDIATE FILAMENTS
12) **FLO:** CRYOGLOBULIN WITH ANTI-IGG ACTIVITY; B IDIOTYPE
13) **LOP:** CRYOGLOBULIN WITH ANTI-IGG ACTIVITY; B IDIOTYPE
14) **SCA:** CRYOGLOBULIN WITH ANTI-LOW-DENSITY LIPOPROTEIN ACTIVITY; B IDIOTYPE
15) **GLO:** ANTI-HUMAN GAMMA G GLOBULIN; WA IDIOTYPE; CRYOGLOBULIN WITH ANTI-IGG ACTIVITY; B IDIOTYPE
18) **MA:** COLD AGGLUTININ WITH ANTI-BLOOD GROUP I ACTIVITY (GROUP 1)
19) **NIC:** COLD AGGLUTININ WITH ANTI-BLOOD GROUP SMALL I ACTIVITY
20) **CUR:** CRYOGLOBULIN WITH ANTI-IGG ACTIVITY; B IDIOTYPE
22) **DRE:** COLD AGGLUTININ WITH ANTI-BLOOD GROUP I ACTIVITY
23) **PER:** COLD AGGLUTININ WITH ANTI-BLOOD GROUP I ACTIVITY
25) **STE:** COLD AGGLUTININ WITH ANTI-BLOOD GROUP I ACTIVITY
26) **GJ:** COLD AGGLUTININ WITH ANTI-BLOOD GROUP I ACTIVITY (ATYPICAL)
27) **TAK:** COLD AGGLUTININ WITH ANTI-BLOOD GROUP I ACTIVITY
35) **AJ:** COLD AGGLUTININ WITH ANTI-BLOOD GROUP I ACTIVITY
42) **CLA:** CRYOGLOBULIN WITH ANTI-IGG ACTIVITY; B IDIOTYPE
43) **SHE':** CRYOGLOBULIN WITH ANTI-IGG ACTIVITY; B IDIOTYPE
48) **POM:** ANTI-HUMAN GAMMA G1 GLOBULIN; PO IDIOTYPE
54) **GOEII:** ANTI-MEASLES VIRUS (WOODFOLK STRAIN); ANTI-SUBACUTE SCLEROSING PANENCEPHALITIS VIRUS (LEC STRAIN)
62) **TEH:** ANTI-HUMAN GAMMA G GLOBULIN
63) **CRA(III):** ANTI-HUMAN GAMMA G GLOBULIN
64) **PLA:** ANTI-HUMAN GAMMA G GLOBULIN
65) **PIN:** ANTI-HUMAN GAMMA G GLOBULIN
70) **BOR:** COLD AGGLUTININ WITH ANTI-BLOOD GROUP I ACTIVITY
71) **DRI:** ANTI-HUMAN GAMMA G GLOBULIN
72) **WAL:** ANTI-HUMAN GAMMA G GLOBULIN
73) **GOL:** ANTI-HUMAN GAMMA G GLOBULIN
74) **GAG:** COLD AGGLUTININ WITH ANTI-BLOOD GROUP I ACTIVITY

CLASS: HUMAN KAPPA LIGHT CHAINS SUBGROUP III

5) **NEU:** IGM-KAPPA
6) **GOT:** IGM-KAPPA
7) **PAY:** IGM-KAPPA
8) **SON:** IGM-KAPPA
9) **WEI':** IGM-KAPPA
10) **GAR':** IGM-KAPPA
11) **PIE:** IGM-KAPPA
12) **FLO:** IGM-KAPPA
13) **LOP:** IGM-KAPPA
14) **SCA:** IGM-KAPPA
15) **GLO:** IGM-KAPPA
20) **CUR:** IGM-KAPPA
42) **CLA:** IGM-KAPPA
43) **SHE':** IGM-KAPPA

REFERENCE: HUMAN KAPPA LIGHT CHAINS SUBGROUP III

1) **TI:** SUTER,L.,BARNIKOL,H.U.,WATANABE,S. & HILSCHMANN,N. (1969) Z.PHYSIOL.CHEM.,350,275-278; (1972) Z.PHYSIOL.CHEM.,353,189-208. (CHECKED BY AUTHOR)
2) **WOL:** ANDREWS,D.W. & CAPRA,J.D. (1981) PROC.NAT.ACAD.SCI.USA,78,3799-3803. (CHECKED BY AUTHOR 08/25/81); ANDREWS,D.W. & CAPRA,J.D. (1981) BIOCHEMISTRY,20,5816-5822.
3) **SIE:** CAPRA,J.D. (1975) ADV.IMMUNOLOGY,20,1-40. (CHECKED BY AUTHOR); ANDREWS,D.W. & CAPRA,J.D. (1981) PROC.NAT.ACAD.SCI.USA,78,3799-3803. (CHECKED BY AUTHOR 08/25/81 WHO SUGGESTED THAT THE SEQUENCE DETERMINED IN 1975 WAS INCORRECT AND SHOULD BE DELETED); ANDREWS,D.W. & CAPRA,J.D. (1981) BIOCHEMISTRY,20,5816-5822.
4) **NG9'CL:** BENTLEY,D.L. (1984) NATURE,307,77-80.
5) **NEU:** LEDFORD,D.K.,GONI,F.,PIZZOLATO,M.,FRANKLIN,E.C.,SOLOMON,A. & FRANGIONE,B. (1983) J.IMMUNOL.,131,1322-1325. (CHECKED BY AUTHOR 03/23/84); GONI,F.,CHEN,P.P.,PONS-ESTEL,B.,CARSON,D.A. & FRANGIONE,B. (1985) J.IMMUNOL.,135,4073-4079.
6) **GOT:** LEDFORD,D.K.,GONI,F.,PIZZOLATO,M.,FRANKLIN,E.C.,SOLOMON,A. & FRANGIONE,B. (1983) J.IMMUNOL.,131,1322-1325. (CHECKED BY AUTHOR 03/23/84); PONS-ESTEL,B.,GONI,F.,SOLOMON,A. & FRANGIONE,B. (1984) J.EXP.MED.,160,893-904; GONI,F.,CHEN,P.P.,PONS-ESTEL,B.,CARSON,D.A. & FRANGIONE,B. (1985) J.IMMUNOL.,135,4073-4079.
7) **PAY:** LEDFORD,D.K.,GONI,F.,PIZZOLATO,M.,FRANKLIN,E.C.,SOLOMON,A. & FRANGIONE,B. (1983) J.IMMUNOL.,131,1322-1325. (CHECKED BY AUTHOR 03/23/84); GONI,F.,CHEN,P.P.,PONS-ESTEL,B.,CARSON,D.A. & FRANGIONE,B. (1985) J.IMMUNOL.,135,4073-4079.
8) **SON:** LEDFORD,D.K.,GONI,F.,PIZZOLATO,M.,FRANKLIN,E.C.,SOLOMON,A. & FRANGIONE,B. (1983) J.IMMUNOL.,131,1322-1325. (CHECKED BY AUTHOR 03/23/84); PONS-ESTEL,B.,GONI,F.,SOLOMON,A. & FRANGIONE,B. (1984) J.EXP.MED.,160,893-904.
9) **WEI':** LEDFORD,D.K.,GONI,F.,PIZZOLATO,M.,FRANKLIN,E.C.,SOLOMON,A. & FRANGIONE,B. (1983) J.IMMUNOL.,131,1322-1325. (CHECKED BY AUTHOR 03/23/84)
10) **GAR':** LEDFORD,D.K.,GONI,F.,PIZZOLATO,M.,FRANKLIN,E.C.,SOLOMON,A. & FRANGIONE,B. (1983) J.IMMUNOL.,131,1322-1325. (CHECKED BY AUTHOR 03/23/84); PONS-ESTEL,B.,GONI,F.,SOLOMON,A. & FRANGIONE,B. (1984) J.EXP.MED.,160,893-904; GONI,F.,CHEN,P.P.,PONS-ESTEL,B.,CARSON,D.A. & FRANGIONE,B. (1985) J.IMMUNOL.,135,4073-4079.
11) **PIE:** PONS-ESTEL,B.,GONI,F.,SOLOMON,A. & FRANGIONE,B. (1984) J.EXP.MED.,160,893-904. (CHECKED BY AUTHOR 05/16/86)
12) **FLO:** LEDFORD,D.K.,GONI,F.,PIZZOLATO,M.,FRANKLIN,E.C.,SOLOMON,A. & FRANGIONE,B. (1983) J.IMMUNOL.,131,1322-1325. (CHECKED BY AUTHOR 03/23/84); GONI,F.,CHEN,P.P.,PONS-ESTEL,B.,CARSON,D.A. & FRANGIONE,B. (1985) J.IMMUNOL.,135,4073-4079.
13) **LOP:** LEDFORD,D.K.,GONI,F.,PIZZOLATO,M.,FRANKLIN,E.C.,SOLOMON,A. & FRANGIONE,B. (1983) J.IMMUNOL.,131,1322-1325. (CHECKED BY AUTHOR 03/23/84)
14) **SCA:** LEDFORD,D.K.,GONI,F.,PIZZOLATO,M.,FRANKLIN,E.C.,SOLOMON,A. & FRANGIONE,B. (1983) J.IMMUNOL.,131,1322-1325. (CHECKED BY AUTHOR 03/23/84)
15) **GLO:** CAPRA,J.D. (1975) ADV.IMMUNOLOGY,20,1-40. (CHECKED BY AUTHOR); LEDFORD,D.K.,GONI,F.,PIZZOLATO,M.,FRANKLIN,E.C.,SOLOMON,A. & FRANGIONE,B. (1983) J.IMMUNOL.,131,1322-1325. (CHECKED BY AUTHOR 03/23/84); GONI,F.,CHEN,P.P.,PONS-ESTEL,B.,CARSON,D.A. & FRANGIONE,B. (1985) J.IMMUNOL.,135,4073-4079.
16) **SAL:** CAPRA,J.D.,KEHOE,J.M.,WINCHESTER,R.J. & KUNKEL,H.G. (1971) ANN.N.Y.ACAD.SCI.,190,371-381. (CHECKED BY AUTHOR)
17) **WIL:** CAPRA,J.D.,KEHOE,J.M.,WINCHESTER,R.J. & KUNKEL,H.G. (1971) ANN.N.Y.ACAD.SCI.,190,371-381. (CHECKED BY AUTHOR)
18) **MA:** CAPRA,J.D.,KEHOE,J.M.,WILLIAMS,R.C.,JR.,FEIZI,T. & KUNKEL,H.G. (1972) PROC.NAT.ACAD.SCI.USA,69,40-43. (CHECKED BY AUTHOR)
19) **NIC:** CAPRA,J.D.,KEHOE,J.M.,WILLIAMS,R.C.,JR.,FEIZI,T. & KUNKEL,H.G. (1972) PROC.NAT.ACAD.SCI.USA,69,40-43. (CHECKED BY AUTHOR)
20) **CUR:** LEDFORD,D.K.,GONI,F.,PIZZOLATO,M.,FRANKLIN,E.C.,SOLOMON,A. & FRANGIONE,B. (1983) J.IMMUNOL.,131,1322-1325. (CHECKED BY AUTHOR 03/23/84); GONI,F.,CHEN,P.P.,PONS-ESTEL,B.,CARSON,D.A. & FRANGIONE,B. (1985) J.IMMUNOL.,135,4073-4079.
21) **FR4:** MILSTEIN,C. (1969) FEBS LETTERS,2,301-304. (CHECKED BY AUTHOR WHO PROVIDED ADDITIONAL RESIDUES TO THOSE PUBLISHED)
22) **DRE:** GERGELY,J.,WANG,A.C. & FUDENBERG,H.H. (1973) VOX SANG.,24,432-440. (CHECKED BY AUTHOR)
23) **PER:** GERGELY,J.,WANG,A.C. & FUDENBERG,H.H. (1973) VOX SANG.,24,432-440. (CHECKED BY AUTHOR)
24) **CAM:** HOPPER,J.E.,NOYES,C.,HSU,R.,HEINRIKSON,R. & GALLAGHER,W. (1979) J.IMMUNOL.,122,2007-2010. (CHECKED BY AUTHOR 01/26/83)
25) **STE:** EDMAN,P. & COOPER,A.G. (1968) FEBS LETTERS,2,33-35. (CHECKED BY AUTHOR)
26) **GJ:** CAPRA,J.D.,KEHOE,J.M.,WILLIAMS,R.C.,JR.,FEIZI,T. & KUNKEL,H.G. (1972) PROC.NAT.ACAD.SCI.USA,69,40-43. (CHECKED BY AUTHOR)
27) **TAK:** GERGELY,J.,WANG,A.C. & FUDENBERG,H.H. (1973) VOX SANG.,24,432-440. (CHECKED BY AUTHOR)
28) **IARC/BL41'CL:** KLOBECK,H.G.,MEINDL,A.,COMBRIATO,G.,SOLOMON,A. & ZACHAU,H.G. (1985) NUC.ACIDS RES.,13,6499-6513.
29) **RAD:** MILSTEIN,C. (1969) FEBS LETTERS,2,301-304. (CHECKED BY AUTHOR)
30) **DIL:** DAYHOFF,M.O. (1972) ATLAS OF PROTEIN SEQUENCE & STRUCTURE,5,D-250. SUBMITTED BY SMITHIES,O.,GIBSON,D.M. AND FANNING,E.M. (CHECKED BY AUTHOR 07/24/79)

REFERENCE: HUMAN KAPPA LIGHT CHAINS SUBGROUP III (cont'd)

31) **CAS:** NIALL,H.D. & EDMAN,P. (1967) NATURE,216,262-263. (CHECKED BY AUTHOR 07/25/79)

32) **MCE':** MIDDAUGH,C.R.,KEHOE,J.M.,PRYSTOWSKY,M.B.,GERBER-JENSON,B.,JENSON,J.C. & LITMAN,G.W. (1978) IMMUNOCHEM.,15,171-187. (CHECKED BY AUTHOR 10/22/80)

33) **KEA:** WANG,A.C. & FUDENBERG,H.H. (1975) IMMUNOL.COMMUN.,4,483-497. (CHECKED BY AUTHOR 09/23/77); WANG,A.C.,TUNG,E.,WANG,I.,FUDENBERG, H.H.,PICK,A.I. & FROEHLICHMAN,R. (1980) CANCER IMMUNOL.IMMUNOTHER.,9,81-86. (CHECKED BY AUTHOR 03/18/81)

34) **SMI:** NIALL,H.D. & EDMAN,P. (1967) NATURE,216,262-263. (CHECKED BY AUTHOR 07/25/79)

35) **AJ:** CAPRA,J.D.,KEHOE,J.M.,WILLIAMS,R.C.,JR.,FEIZI,T. & KUNKEL,H.G. (1972) PROC.NAT.ACAD.SCI.USA,69,40-43. (CHECKED BY AUTHOR)

36) **BRO'IGG:** HOPPER,J.E.,NOYES,C.,HEINRIKSON,R. & KESSEL,J.W. (1976) J.IMMUNOL.,116,743-746. (CHECKED BY AUTHOR 01/26/83)

37) **NIG:** NIALL,H.D. & EDMAN,P. (1967) NATURE,216,262-263. (CHECKED BY AUTHOR 07/25/79)

38) **IKE:** CAPRA,J.D. (1975) ADV.IMMUNOLOGY,20,1-40. (CHECKED BY AUTHOR)

39) **TIL:** PINK,J.R.L.,WANG,A.C. & FUDENBERG,H.H. (1971) ANN.REV.MED.,22,145-170. (CHECKED BY AUTHOR)

40) **AMYLOID KSA:** SLETTEN,K.,WESTERMARK,P.,PITKANEN,P.,THYRESSON,N. & OLSTAD,O.K. (1983) SCAND.J.IMMUNOL.,18,557-560. (CHECKED BY AUTHOR 04/26/84)

41) **POL:** WANG,A.C.,WELLS,J.V.,FUDENBERG,H.H. & GERGELY,J. (1974) IMMUNOCHEM.,11,341-345. (CHECKED BY AUTHOR)

42) **CLA:** LEDFORD,D.K.,GONI,F.,PIZZOLATO,M.,FRANKLIN,E.C.,SOLOMON,A. & FRANGIONE,B. (1983) J.IMMUNOL.,131,1322-1325. (CHECKED BY AUTHOR 03/23/84)

43) **SHE':** LEDFORD,D.K.,GONI,F.,PIZZOLATO,M.,FRANKLIN,E.C.,SOLOMON,A. & FRANGIONE,B. (1983) J.IMMUNOL.,131,1322-1325. (CHECKED BY AUTHOR 03/23/84)

44) **JH:** JEMMERSON,R.,KAPLAN,B.,DENTON,M.D.,ANDERAS,P.,ANDERSON,B. & MARGOLIASH,E. (1979) BIOCHEMISTRY,18,4676-4683.

45) **WIN:** NIALL,H.D. & EDMAN,P. (1967) NATURE,216,262-263. (CHECKED BY AUTHOR 07/25/79)

46) **LEA:** WANG,A.C.,WELLS,J.V.,FUDENBERG,H.H. & GERGELY,J. (1974) IMMUNOCHEM.,11,341-345. (CHECKED BY AUTHOR)

47) **ARP:** WANG,A.C.,TUNG,E.,WANG,I.,FUDENBERG,H.H.,PICK,A.I. & FROEHLICHMAN,R. (1980) CANCER IMMUNOL.IMMUNOTHER.,9,81-86. (CHECKED BY AUTHOR 03/18/81)

48) **POM:** KLAPPER,D.G. & CAPRA,J.D. (1976) ANN.IMMUNOL.(INST.PASTEUR),127C,261-271. (CHECKED BY AUTHOR 08/01/79)

49) **VAND:** SEON,B.K.,GAILANI,S.,HENDERSON,E.S. & PRESSMAN,D. (1977) IMMUNOCHEM.,14,567-572. (CHECKED BY AUTHOR 08/28/78)

50) **AMYLOID SO124:** SLETTEN,K.,WESTERMARK,P.,PITKANEN,P.,THYRESSON,N. & OLSTAD,O.K. (1983) SCAND.J.IMMUNOL.,18,557-560. (CHECKED BY AUTHOR 04/26/84)

51) **DOV:** WANG,A.C.,TUNG,E.,WANG,I.,FUDENBERG,H.H.,PICK,A.I. & FROEHLICHMAN,R. (1980) CANCER IMMUNOL.IMMUNOTHER.,9,81-86. (CHECKED BY AUTHOR 03/18/81)

52) **SHM:** WANG,A.C.,TUNG,E.,WANG,I.,FUDENBERG,H.H.,PICK,A.I. & FROEHLICHMAN,R. (1980) CANCER IMMUNOL.IMMUNOTHER.,9,81-86. (CHECKED BY AUTHOR 03/18/81)

53) **GRA:** NIALL,H.D. & EDMAN,P. (1967) NATURE,216,262-263. (CHECKED BY AUTHOR 07/25/79)

54) **GOEII:** STROSBERG,A.D.,KARCHER,D. & LOWENTHAL,A. (1975) J.IMMUNOL.,115,157-160. (CHECKED BY AUTHOR)

55) **LOW':** WANG,A.C.,TUNG,E.,WANG,I.,FUDENBERG,H.H.,PICK,A.I. & FROEHLICHMAN,R. (1980) CANCER IMMUNOL.IMMUNOTHER.,9,81-86. (CHECKED BY AUTHOR 03/18/81)

56) **VER:** CHERSI,A. & NATALI,P.G. (1978) IMMUNOCHEMISTRY,15,585-589. (CHECKED BY AUTHOR 09/13/79)

57) **REE:** PRELLI,F.,TUMMOLO,D.,SOLOMON,A. & FRANGIONE,B. (1986) J.IMMUNOL., IN PRESS.

58) **WE:** DWORSKY,E.,SLETTEN,K.,HARBOE,M. & WETTELAND,P. (1980) SCAND.J.IMMUNOL.,12,281-287. (CHECKED BY AUTHOR 02/28/1984)

59) **HOW:** KAPLAN,A.P. & METZGER,H. (1969) BIOCHEMISTRY,8,3944-3951. (CHECKED BY AUTHOR)

60) **HS4:** HOOD,L.,GRAY,W.R.,SANDERS,B.G. & DREYER,W.J. (1967) COLD SPRING HARBOR SYMP. QUANTITATIVE BIOL.,32,133-145.

61) **HBJ5:** HOOD,L.,GRAY,W.R.,SANDERS,B.G. & DREYER,W.J. (1967) COLD SPRING HARBOR SYMP. QUANTITATIVE BIOL.,32,133-145.

62) **TEH:** JOHNSTON,S.L.,ABRAHAM,G.N. & WELCH,E.H. (1975) BIOCHEM.BIOPHYS.RES.COMMUN.,66,842-847. (CHECKED BY AUTHOR 10/17/77)

63) **CRA(III):** JOHNSTON,S.L.,ABRAHAM,G.N. & WELCH,E.H. (1975) BIOCHEM.BIOPHYS.RES.COMMUN.,66,842-847. (CHECKED BY AUTHOR 10/17/77)

64) **PLA:** JOHNSTON,S.L.,ABRAHAM,G.N. & WELCH,E.H. (1975) BIOCHEM.BIOPHYS.RES.COMMUN.,66,842-847. (CHECKED BY AUTHOR 10/17/77)

65) **PIN:** JOHNSTON,S.L.,ABRAHAM,G.N. & WELCH,E.H. (1975) BIOCHEM.BIOPHYS.RES.COMMUN.,66,842-847. (CHECKED BY AUTHOR 10/17/77)

66) **MCE:** CAPRA,J.D.,KEHOE,J.M.,WILLIAMS,R.C.,JR.,FEIZI,T. & KUNKEL,H.G. (1972) PROC.NAT.ACAD.SCI.USA,69,40-43. (CHECKED BY AUTHOR)

67) **HAC:** HOOD,L. & TALMAGE,D.W. (1970) SCIENCE,168,325-334.

68) **K- EV15'CL:** STAVNEZER,J.,KEKISH,O.,BATTER,D.,GRENIER,J.,BALAZS,I.,HENDERSON,E. & ZEGERS,B.J.M. (1985) NUC.ACIDS RES.,13,3495-3514.

69) **BER:** WANG,A.C.,WELLS,J.V.,FUDENBERG,H.H. & GERGELY,J. (1974) IMMUNOCHEM.,11,341-345. (CHECKED BY AUTHOR)

70) **BOR:** GERGELY,J.,WANG,A.C. & FUDENBERG,H.H. (1973) VOX SANG.,24,432-440. (CHECKED BY AUTHOR)

71) **DRI:** CAPRA,J.D. (1975) ADV.IMMUNOLOGY,20,1-40. (CHECKED BY AUTHOR)

72) **WAL:** CAPRA,J.D. (1975) ADV.IMMUNOLOGY,20,1-40. (CHECKED BY AUTHOR)

73) **GOL:** CAPRA,J.D. (1975) ADV.IMMUNOLOGY,20,1-40. (CHECKED BY AUTHOR)

74) **GAG:** CAPRA,J.D.,KEHOE,J.M.,WILLIAMS,R.C.,JR.,FEIZI,T. & KUNKEL,H.G. (1972) PROC.NAT.ACAD.SCI.USA,69,40-43. (CHECKED BY AUTHOR)

75) **DOB:** HOOD,L. & TALMAGE,D.W. (1970) SCIENCE,168,325-334.

76) **HS6:** HOOD,L.,GRAY,W.R.,SANDERS,B.G. & DREYER,W.J. (1967) COLD SPRING HARBOR SYMP. QUANTITATIVE BIOL.,32,133-145.

77) **HBJ12:** HOOD,L.,GRAY,W.R.,SANDERS,B.G. & DREYER,W.J. (1967) COLD SPRING HARBOR SYMP. QUANTITATIVE BIOL.,32,133-145.

78) **BUR(K):** MOULIN,A. & FOUGEREAU,M. (1973) NATURE NEW BIOLOGY,246,176-178. (CHECKED BY AUTHOR)

79) **LEG:** MOULIN,A. & FOUGEREAU,M. (1973) NATURE NEW BIOLOGY,246,176-178. (CHECKED BY AUTHOR)

80) **B6:** MILSTEIN,C. (1969) FEBS LETTERS,2,301-304. (CHECKED BY AUTHOR)

81) **AMYLOID WR:** WESTERMARK,P.,SLETTEN,K.,PITKANEN,P.,NATVIG,J.B. & LINDHOLM,C.E. (1982) MOL.IMMUNOL.,19,447-450. (CHECKED BY AUTHOR 06/01/83)

82) **VKAPPA3'CL:** BENTLEY,D.L. & RABBITTS,T.H. (1981) CELL,24,613-623. (CHECKED BY AUTHOR 12/07/81)

NOTES: HUMAN KAPPA LIGHT CHAINS SUBGROUP III

IDENTICAL SETS OF FRAMEWORK SEGMENTS:

FR1:
- SET 1: TI[1],WOL[2],SIE[3],NG9'CL[4],NEU[5],GOT[6],PAY[7],SON[8],WEI'[9],GAR'[10],PIE[11],FLO[12],LOP[13],SCA[14],GLO[15],SAL[16], WIL[17],MA[18],NIC[19],CUR[20],FR4[21],DRE[22],PER[23],CAM[24]. (24 IDENTICAL)
- SET 2: GJ[26],TAK[27]. (2 IDENTICAL)
- SET 3: RAD[29],DIL[30],CAS[31]. (3 IDENTICAL)
- SET 4: KEA[33],SMI[34]. (2 IDENTICAL HUMAN V-KAPPA-III; ALSO 1 MOUSE V-KAPPA-V: Vg'CL[122].)
- SET 5: DRE[22],PER[23],BRO'IGG[36]. (3 IDENTICAL)
- SET 6: CLA[42],SHE'[43]. (2 IDENTICAL)

FR2:
- SET 1: TI[1],WOL[2],SIE[3],NG9'CL[4],NEU[5],GOT[6],SON[8],GAR'[10],PIE[11],FLO[12],GLO[15],CUR[20]. (12 IDENTICAL HUMAN V-KAPPA-III; ALSO 1 MOUSE V-KAPPA-IV: Vh'CL[12]; AND 1 MOUSE V-KAPPA-V: Vg'CL[122].)

FR3:
- SET 1: TI[1],WOL[2]. (2 IDENTICAL)
- SET 2: GOT[6],PAY[7],GAR'[10],PIE[11],FLO[12],GLO[15],CUR[20]. (7 IDENTICAL)

FR4:
- SET 1: WOL[2],PAY[7],PIE[11],GLO[15],CUR[20],REE[57],VKAPPA3'CL[82]. (7 IDENTICAL HUMAN V-KAPPA-III; ALSO 3 HUMAN V-KAPPA-I: AU[2],GAL(I)[36],CL'[110]; 2 HUMAN V-KAPPA-II: GM 607 'CL[5],RPM1-6410'CL[16]; AND 1 HUMAN V-KAPPA-IV: PB17IV'CL[3].)
- SET 2: POM[48]. (IDENTICAL TO 1 HUMAN V-KAPPA-I: HAU[4].)
- SET 3: NEU[5],GOT[6],GAR'[10],FLO[12],FR4[21],IARC/BL41'CL[28]. (6 IDENTICAL HUMAN V-KAPPA-III; ALSO 3 HUMAN V-KAPPA-I: AG[7], DEN[46],BI[63]; 2 HUMAN V-KAPPA-II: NIM[3],FR[14]; AND 1 HUMAN V-KAPPA-IV: LEN[4].)
- SET 4: SON[8]. (IDENTICAL TO 1 HUMAN V-KAPPA-IV: VJI'CL[1].)

IDENTICAL SETS OF COMPLEMENTARITY DETERMINING REGIONS:

CDR1:
- SET 1: SIE[3],IKE[38]. (2 IDENTICAL)
- SET 2: NG9'CL[4],PAY[7],SON[8],WEI'[9],GAR'[10],PIE[11],FLO[12],GLO[15],CUR[20],DRE[22],CAM[24]. (11 IDENTICAL)
- SET 3: TIL[39]. (IDENTICAL TO 1 MOUSE V-KAPPA-V: Vg'CL[122].)

CDR2:
- SET 1: WOL[2],SIE[3],NEU[5],GOT[6],PAY[7],SON[8],GAR'[10],PIE[11],FLO[12],GLO[15],CUR[20]. (11 IDENTICAL)
- SET 2: POM[48]. (IDENTICAL TO 1 MOUSE V-KAPPA-IV: Vh'CL[12].)

CDR3:
- SET 1: POM[48]. (IDENTICAL TO 1 HUMAN V-KAPPA-I: LAY[39].)
- SET 2: GOT[6],CUR[20]. (2 IDENTICAL)
- SET 3: PAY[7],GLO[15]. (2 IDENTICAL)
- SET 4: GAR'[10],FLO[12]. (2 IDENTICAL)

IDENTICAL SETS OF J-MINIGENES:
- SET 1: PIE[11],VKAPPA3'CL[82]. (2 IDENTICAL HUMAN V-KAPPA-III; ALSO 1 HUMAN V-KAPPA-I: AU[2]; 1 HUMAN V-KAPPA-II: RPM1-6410'CL[16]; AND 1 HUMAN V-KAPPA-IV: PB17IV'CL[3].)
- SET 2: GOT[6]. (IDENTICAL TO 1 HUMAN V-KAPPA-I: AG[7].)
- SET 3: GAR'[10],FLO[12],IARC/BL41'CL[28]. (3 IDENTICAL HUMAN V-KAPPA-III; ALSO 2 HUMAN V-KAPPA-I: DEN[46],BI[63]; AND 1 HUMAN V-KAPPA-II: FR[14].)
- SET 4: WOL[2],CUR[20]. (2 IDENTICAL)
- SET 5: PAY[7],GLO[15]. (2 IDENTICAL)

SPECIFIC NOTES:

4) **NG9'CL:** THE AMINO ACID SEQUENCE IS TRANSLATED FROM THE NUCLEOTIDE SEQUENCE OF A CLONE OF HUMAN CDNA.

32) **MCE':** IT IS A CRYOIMMUNOGLOBULIN. THE AUTHORS ORIGINALLY DESIGNATED IT AS MCE, BUT IN ORDER TO DIFFERENTIATE IT FROM ANOTHER MCE SEQUENCED BY CAPRA ET AL., IT IS DENOTED AS MCE'.

42) **CLA:** THE AMINO ACID RESIDUES FOUND AT POSITION 9 WERE GLY AND ALA.

43) **SHE':** THE AMINO ACID RESIDUES FOUND AT POSITION 9 WERE GLY AND ALA.

NOTES: HUMAN KAPPA LIGHT CHAINS SUBGROUP III (cont'd)

44) **JH:** THE NAME WAS GIVEN TO US BY THE AUTHORS. IT IS NOT INCLUDED IN THE PAPER.

58) **WE:** AT POSITIONS 20,29 AND 33 OF AMINO ACID SEQUENCE WERE FOUND BOTH LEU AND ILE. IN THE SAME SEQUENCE TWO RESIDUES WERE FOUND IN POSITIONS 1,3,4,9,10,15,17,19,20,21,22 AND 29. THE SECOND RESIDUES WERE GLU,VAL,LEU,GLY,THR,PRO,GLU,ALA,THR,LEU,SER AND VAL, RESPECTIVELY. A DETERMINATION WAS NOT MADE IN THE ARTICLE AS TO WHETHER THE SEQUENCE BELONGED TO SUBGROUP I OR TO SUBGROUP III.

81) **AMYLOID WR:** AMINO ACID RESIDUES FOUND AT POSITION 54 ARE LEU AND ALA.

82) **VKAPPA3'CL:** THE AMINO ACID SEQUENCE IS OBTAINED BY TRANSLATING THE NUCLEOTIDE SEQUENCE OF A CLONE OF CDNA FROM A MOUSE-HUMAN HYBRID CELL LINE.

HUMAN KAPPA LIGHT CHAINS SUBGROUP IV

		INVARIANT RESIDUES	1 VJI °CL	2 VKAPPA IV GERMLINE °CL	3* PB17IV °CL	4 LEN	5* R.K.	6* L. TH.	7* TUR	8 AH	9 DA	10 DA-H	11 DA-N	12 JAH	13 SCH	14 JUV	15 AMYLOID GAB	# OF SEQUENCES	# OF AMINO ACIDS
	0		---	---	---	---	---	---	---	---	---	---	---	---	---	---	---	15	1
	1	ASP	ASP	ASP	ASP	ASP	ASP	ASP	ASP	ASP	ASP	ASP	ASP	ASP	ASP	ASP	ASP	15	2
	2		ILE	ILE	ILE	ILE	ILE	ILE	VAL	VAL	VAL	VAL	ILE	VAL	VAL	leu	ILE	15	1
	3	VAL	VAL	VAL	VAL	VAL	VAL	VAL	VAL	VAL	VAL	VAL	VAL	VAL	VAL	VAL	VAL	15	2
	4		MET	MET	MET	MET	MET	leu	MET	MET	MET	MET	leu	MET	MET	MET	MET	15	2
	5		THR	THR	THR	THR	THR	THR	THR	THR	THR	THR	gln	THR	THR	THR	THR	15	1
	6	GLN	GLN	GLN	GLN	GLN	GLN	GLN	GLN	GLN	GLN	GLN	GLN	GLN	GLN	GLN	GLN	14	1
	7	SER	SER	SER	SER	SER	SER	SER	SER	SER	SER	SER	SER	SER	SER	SER		15	1
	8	PRO	PRO	PRO	PRO	PRO	PRO	PRO	PRO	PRO	PRO	PRO	PRO	PRO	PRO	PRO	PRO	15	1
	9		ASP	ASP	ASP	asn	ASX	ASX	ser	glx	ASP	ASP	ASP	ASP	ala	asn	ASX	15	5
FR1	10		SER	SER	SER	SER	SER	SER	SER	SER	SER	SER	SER	thr	thr			13	2
	11	LEU	LEU	LEU	LEU	LEU	LEU	LEU	LEU	LEU	LEU	LEU	LEU	LEU	LEU	LEU		14	1
	12	ALA	ALA	ALA	ALA	ALA	ALA	ALA	ALA	ALA	ALA	ALA	ALA	ALA	ALA	ALA		14	1
	13	VAL	VAL	VAL	VAL	VAL	VAL	VAL	VAL	VAL	VAL	VAL	VAL	VAL	VAL	VAL		14	1
	14	SER	SER	SER	SER	SER	SER	SER	SER	SER	SER	SER	SER					11	1
	15		LEU	LEU	LEU	LEU	LEU	LEU	LEU	pro	pro	pro	LEU					11	2
	16	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY					11	1
	17		GLU	GLU	GLU	GLU	GLX	GLX	GLU	asp	asp	asp	asp					11	2 : 3
	18		ARG	ARG	ARG	ARG	ARG	ARG	ARG	ARG	gln	gln	leu					11	3
	19	ALA	ALA	ALA	ALA	ALA	ALA	ALA	ALA	ALA	ALA	ALA	ALA				ALA	12	1
	20	THR	THR	THR	THR	THR	THR	THR	THR	THR	THR	THR	THR				THR	12	1
	21		ILE	ILE	ILE	ILE	ILE	ILE	ILE	ILE	val	val	leu				ILE	12	3
	22		ASN	ASN	ASN	ASN	ASX	ASX	ser	ASX	ser	ser	ser				asp	12	3
	23	CYS	CYS	CYS	CYS	CYS			CYS	CYS	CYS	CYS	CYS				CYS	10	1
	24		LYS	LYS	LYS	LYS			ARG	ARG	GLN	GLN	GLN				LYS	10	3
	25		SER	SER	SER	SER			SER	ARG	ALA	ALA	ALA					9	3
	26		SER	SER	SER	SER			SER	ALA			SER					7	2
	27		GLN	GLN	GLN	GLN			GLN	GLX			GLN					7	1 : 2
	27A		SER	SER	SER	SER			SER	ARG			---					6	2
	27B		VAL	VAL	ILE	VAL			VAL	VAL			VAL					7	2
CDR1	27C	LEU	LEU	LEU	LEU	LEU			LEU				LEU					6	1
	27D	TYR	TYR	TYR	TYR	TYR							TYR					5	1
	27E		SER	SER	SER	SER				TYR								5	2
	27F	SER	SER	SER	SER	SER												4	1
	28		ASN	ASN	ASP	ASN							ASP					5	2
	29		ASN	ASN	ASN	SER												4	2
	30	LYS	LYS	LYS	LYS	LYS							LYS					5	1
	31	ASN	ASN	ASN	ASN	ASN												4	1
	32	TYR	TYR	TYR	TYR	TYR												4	1
	33	LEU	LEU	LEU	LEU	LEU												4	1
	34	ALA	ALA	ALA	ALA	ALA												4	1
	35	TRP	TRP	TRP	TRP	TRP												4	1
	36	TYR	TYR	TYR	TYR	TYR												4	1
	37	GLN	GLN	GLN	GLN	GLN												4	1
	38	GLN	GLN	GLN	GLN	GLN												4	1
	39	LYS	LYS	LYS	LYS	LYS												5	1
	40	PRO	PRO	PRO	PRO	PRO					PRO							5	1
	41	GLY	GLY	GLY	GLY	GLY					GLY							5	1
FR2	42	GLN	GLN	GLN	GLN	GLN					GLN							5	2
	43		PRO	PRO	PRO	PRO					ALA								
	44	PRO	PRO	PRO	PRO	PRO					PRO							5	1
	45	LYS	LYS	LYS	LYS	LYS					LYS							5	1
	46	LEU	LEU	LEU	LEU	LEU					LEU							5	1
	47	LEU	LEU	LEU	LEU	LEU					LEU							5	1
	48	ILE	ILE	ILE	ILE	ILE					ILE							5	1
	49	TYR	TYR	TYR	TYR	TYR					TYR							5	1
	50	TRP	TRP	TRP	TRP	TRP					TRP							5	2
	51		ALA	ALA	ALA	ALA					GLY							5	2
CDR2	52		SER	SER	SER	SER					ARG							4	1
	53	THR	THR	THR	THR	THR													
	54	ARG	ARG	ARG	ARG	ARG												4	1
	55	GLU	GLU	GLU	GLU	GLU												4	1
	56	SER	SER	SER	SER	SER												4	1
	57	GLY	GLY	GLY	GLY	GLY												4	1
	58	VAL	VAL	VAL	VAL	VAL												4	1
	59	PRO	PRO	PRO	PRO	PRO												4	1
	60	ASP	ASP	ASP	ASP	ASP												4	1
	61	ARG	ARG	ARG	ARG	ARG												4	1
	62	PHE	PHE	PHE	PHE	PHE												5	1
	63	SER	SER	SER	SER	SER					SER								
	64	GLY	GLY	GLY	GLY	GLY					GLY							5	1
	65	SER	SER	SER	SER	SER					SER							5	1
	66	GLY	GLY	GLY	GLY	GLY					GLY							5	1
	67	SER	SER	SER	SER	SER					SER							5	1
	68		GLY	GLY	GLY	GLY					LYS							5	2
	69	THR	THR	THR	THR	THR												4	1
	70	ASP	ASP	ASP	ASP	ASP												4	1
	71	PHE	PHE	PHE	PHE	PHE												4	1
FR3	72	THR	THR	THR	THR	THR												4	1
	73	LEU	LEU	LEU	LEU	LEU												4	1
	74	THR	THR	THR	THR	THR												4	1
	75	ILE	ILE	ILE	ILE	ILE												4	1
	76	SER	SER	SER	SER	SER												4	1
	77	SER	SER	SER	SER	SER												4	1
	78	LEU	LEU	LEU	LEU	LEU												4	1
	79	GLN	GLN	GLN	GLN	GLN												4	1
	80	ALA	ALA	ALA	ALA	ALA												4	1
	81	GLU	GLU	GLU	GLU	GLU												4	1
	82	ASP	ASP	ASP	ASP	ASP												4	1
	83	VAL	VAL	VAL	VAL	VAL												4	1
	84	ALA	ALA	ALA	ALA	ALA												4	1
	85	VAL	VAL	VAL	VAL	VAL												4	1
	86	TYR	TYR	TYR	TYR	TYR												4	1
	87	TYR	TYR	TYR	TYR	TYR												4	1
	88	CYS	CYS	CYS	CYS	CYS												4	1
	89	GLN	GLN	GLN	GLN	GLN												4	1
	90	GLN	GLN	GLN	GLN	GLN												4	1
	91	TYR	TYR	TYR	TYR	TYR												4	2
	92		ASP	TYR	TYR	TYR												4	3
	93		THR	SER	ASN	SER												4	3
	94		ILE	THR	LEU	THR												4	1
CDR3	95	PRO	PRO	PRO	PRO	PRO													
	95A		---	---	---	---													
	95B		---	---	---	---													
	95C		---	---	---	---													
	95D		---	---	---	---													
	95E		---	---	---	---													
	95F		---	---	---	---													
	96		---	---	TRP	TYR												2	2
	97		THR	---	THR	SER												3	2
	98	PHE	PHE	---	PHE	PHE												3	1
	99	GLY	GLY	---	GLY	GLY												3	1
	100		GLY	---	GLN	GLN												3	2
	101	GLY	GLY	---	GLY	GLY												3	1
	102	THR	THR	---	THR	THR												3	1
FR4	103	LYS	LYS	---	LYS	LYS												3	1
	104		VAL	---	VAL	LEU						LEU						4	2
	105	GLU	GLU	---	GLU	GLU						GLU						4	1
	106	ILE	ILE	---	ILE	ILE						ILE						4	1
	106A		---	---	---	---						---							
	107		LYS	---	LYS	LYS						ARG						4	2
	108	ARG	ARG	---	ARG	ARG												3	1
	109			---		THR												1	1

HUMAN KAPPA LIGHT CHAINS SUBGROUP IV (cont'd)

		OCCURRENCES OF MOST COMMON AMINO ACID	VARIABILITY
	0		
	1	15(ASP)	1.
	2	14(ILE)	2.1
	3	15(VAL)	1.
	4	13(MET)	2.3
	5	14(THR)	2.1
	6	15(GLN)	1.
	7	14(SER)	1.
	8	15(PRO)	1.
	9	10(ASP) : 7(ASP)	7.5 : 11.
FR1	10	11(SER)	2.4
FR1	11	14(LEU)	1.
FR1	12	14(ALA)	1.
FR1	13	14(VAL)	1.
FR1	14	11(SER)	1.
	15	8(LEU)	2.8
	16	11(GLY)	1.
	17	7(GLU) : 5(GLU)	3.1 : 6.6
	18	8(ARG)	4.1
	19	12(ALA)	1.
	20	12(THR)	1.
	21	9(ILE)	4.
	22	7(ASN) : 4(+)	5.1 : 9.
	23	10(CYS)	1.
	24	5(LYS)	6.
	25	5(SER)	5.4
	26	6(SER)	2.3
	27	7(GLN) : 6(GLN)	1. : 2.3
	27A	5(SER)	
	27B	6(VAL)	
CDR1	27C	6(LEU)	
CDR1	27D	5(TYR)	
CDR1	27E	4(SER)	
CDR1	27F	4(SER)	
CDR1	28	3(ASN)	3.3
	29	3(ASN)	2.7
	30	5(LYS)	1.
	31	4(ASN)	1.
	32	4(TYR)	1.
	33	4(LEU)	1.
	34	4(ALA)	1.
	35	4(TRP)	1.
	36	4(TYR)	1.
	37	4(GLN)	1.
	38	4(GLN)	1.
	39	4(LYS)	1.
	40	5(PRO)	1.
FR2	41	5(GLY)	1.
FR2	42	5(GLN)	1.
FR2	43	4(PRO)	2.5
	44	5(PRO)	1.
	45	5(LYS)	1.
	46	5(LEU)	1.
	47	5(LEU)	1.
	48	5(ILE)	1.
	49	5(TYR)	1.
	50	5(TRP)	1.
	51	4(ALA)	2.5
CDR2	52	4(SER)	2.5
CDR2	53	4(THR)	1.
CDR2	54	4(ARG)	1.
CDR2	55	4(GLU)	1.
CDR2	56	4(SER)	1.
	57	4(GLY)	1.
	58	4(VAL)	1.
	59	4(PRO)	1.
	60	4(ASP)	1.
	61	4(ARG)	1.
	62	4(PHE)	1.
	63	5(SER)	1.
	64	5(GLY)	1.
	65	5(SER)	1.
	66	5(GLY)	1.
	67	5(SER)	1.
	68	4(GLY)	2.5
	69	4(THR)	1.
	70	4(ASP)	1.
FR3	71	4(PHE)	1.
FR3	72	4(THR)	1.
FR3	73	4(LEU)	1.
	74	4(THR)	1.
	75	4(ILE)	1.
	76	4(SER)	1.
	77	4(SER)	1.
	78	4(LEU)	1.
	79	4(GLN)	1.
	80	4(ALA)	1.
	81	4(GLU)	1.
	82	4(ASP)	1.
	83	4(VAL)	1.
	84	4(ALA)	1.
	85	4(VAL)	1.
	86	4(TYR)	1.
	87	4(TYR)	1.
	88	4(CYS)	1.
	89	4(GLN)	1.
	90	4(GLN)	1.
	91	4(TYR)	1.
	92	3(TYR)	2.7
	93	2(SER)	6.
CDR3	94	2(THR)	6.
CDR3	95	4(PRO)	1.
CDR3	95A		
CDR3	95B		
CDR3	95C		
	95D		
	95E		
	95F		
	96	1(+)	4.
	97	2(THR)	3.
	98	3(PHE)	1.
	99	3(GLY)	1.
	100	2(GLN)	3.
	101	3(GLY)	1.
	102	3(THR)	1.
FR4	103	3(LYS)	1.
FR4	104	2(+)	4.
FR4	105	4(GLU)	1.
FR4	106	4(ILE)	1.
FR4	106A		
	107	3(LYS)	2.7
	108	3(ARG)	1.
	109	1(THR)	

ANTIBODY SPECIFICITIES: HUMAN KAPPA LIGHT CHAINS SUBGROUP IV

3) **PB17IV'CL:** ANTI-STREPTOCOCCUS GROUP A CARBOHYDRATE WITH SPECIFICITY FOR N-ACETYL GLUCOSAMINE
5) **R.K.:** COLD AGGLUTININ WITH ANTI-PR1H ACTIVITY (RBC MEMBRANE ANTIGEN ON HUMAN ERYTHROCYTES INACTIVATED BY PROTEOLYTIC ENZYMES AND NEURAMINIDASE)
6) **L.TH.:** COLD AGGLUTININ WITH ANTI-PR2 ACTIVITY (RBC MEMBRANE ANTIGEN ON HUMAN, RAT AND GUINEA PIG ERYTHROCYTES INACTIVATED BY PROTEOLYTIC ENZYMES AND NEURAMINIDASE)
7) **TUR:** COLD AGGLUTININ WITH ANTI-PR ACTIVITY

REFERENCE: HUMAN KAPPA LIGHT CHAINS SUBGROUP IV

1) **VJI'CL:** KLOBECK,H.G.,BORNKAMMM,G.W.,COMBRIATO,G.,MOCIKAT,R.,POHLENZ,H.D. & ZACHAU,H.G. (1985) NUC.ACIDS RES.,13,6515-6529. (CHECKED BY AUTHOR 02/25/86)
2) **VKAPPA IV GERMLINE'CL:** KLOBECK,H.G.,BORNKAMMM,G.W.,COMBRIATO,G.,MOCIKAT,R.,POHLENZ,H.D. & ZACHAU,H.G. (1985) NUC.ACIDS RES.,13, 6515-6529.
3) **PB17IV'CL:** MARSH,P.,MILLS,F. & GOULD,H. (1985) NUC.ACIDS RES.,13,6531-6544. (CHECKED BY AUTHOR 03/19/86 WHO CORRECTED A MISPRINT IN THE ORIGINAL PAPER FOR RESIDUE 50)
4) **LEN:** SCHNEIDER,M. & HILSCHMANN,N. (1974) Z.PHYSIOL.CHEM.,355,1164-1168. (CHECKED BY AUTHOR)
5) **R.K.:** WANG,A.C.,FUDENBERG,H.H.,WELLS,J.V. & ROELCKE,D. (1973) NATURE NEW BIOLOGY,243,126-128. (CHECKED BY AUTHOR)
6) **L.TH.:** WANG,A.C.,FUDENBERG,H.H.,WELLS,J.V. & ROELCKE,D. (1973) NATURE NEW BIOLOGY,243,126-128. (CHECKED BY AUTHOR)
7) **TUR:** CAPRA,J.D.,KEHOE,J.M.,WILLIAMS,R.C.,JR.,FEIZI,T. & KUNKEL,H.G. (1972) PROC.NAT.ACAD.SCI.USA,69,40-43. (CHECKED BY AUTHOR)
8) **AH:** PICK,A.I.,WANG,A.C.,FROHLICHMAN,R. & FUDENBERG,H.H. (1982) ACTA HAEMAT.,68,207-214. (CHECKED BY AUTHOR 05/26/83)
9) **DA:** WANG,A.C.,ZHANG,H.S.,BONEWALD,L.,TUNG,E.,BOUVET,J.P. & LIACOPOULOS,P. (1985) MIAMI WINTER SYMP.,17,335-336. (CHECKED BY AUTHOR 02/25/86 WHO CORRECTED RESIDUES AS SHOWN)
10) **DA-H:** BOUVET,J.P.,LIACOPOULOS,P.,PILLOT,J.,BANDA,R.,TUNG,E. & WANG,A.C. (1980) J.IMMUNOL.,125,213-220. (CHECKED BY AUTHOR 08/04/80); BOUVET,J.P.,LIACOPOULOS,P.,PILLOT,J.,BANDA,R.,TUNG,E. & WANG,A.C. (1982) J.IMMUNOL.,129,1519-1524.
11) **DA-N:** BOUVET,J.P.,LIACOPOULOS,P.,PILLOT,J.,BANDA,R.,TUNG,E. & WANG,A.C. (1980) J.IMMUNOL.,125,213-220. (CHECKED BY AUTHOR 08/04/80); BOUVET,J.P.,LIACOPOULOS,P.,PILLOT,J.,BANDA,R.,TUNG,E. & WANG,A.C. (1982) J.IMMUNOL.,129,1519-1524.
12) **JAH:** SLETTEN,K.,HANNESTAD,K. & HARBOE,M. (1974) SCAND.J.IMMUNOL.,3,219-222. (CHECKED BY AUTHOR 12/05/77)
13) **SCH:** SLETTEN,K.,HANNESTAD,K. & HARBOE,M. (1974) SCAND.J.IMMUNOL.,3,219-222. (CHECKED BY AUTHOR 12/05/77)
14) **JUV:** SLETTEN,K.,HANNESTAD,K. & HARBOE,M. (1974) SCAND.J.IMMUNOL.,3,219-222. (CHECKED BY AUTHOR 12/05/77)
15) **AMYLOID GAB:** PRAS,M.,FRANGIONE,B. & FRANKLIN,E.C. (1980) IN AMYLOID AND AMYLOIDOSIS,G.G.GLENNER,P.P.E COSTA & F.DE FREITAS EDS., EXCERPTA MEDICA AMSTERDAM OXFORD-PRINCETON,249-252. (CHECKED BY AUTHOR 11/18/81)

NOTES: HUMAN KAPPA LIGHT CHAINS SUBGROUP IV

IDENTICAL SETS OF FRAMEWORK SEGMENTS:

FR1: SET 1: VJI'CL[1],VKAPPA IV GERMLINE'CL[2],PB17IV'CL[3],R.K.[5]. (4 IDENTICAL)
SET 2: LEN[4],R.K.[5]. (2 IDENTICAL)
SET 3: DA[9],DA-H[10]. (2 IDENTICAL)

FR2: SET 1: VJI'CL[1],VKAPPA IV GERMLINE'CL[2],PB17IV'CL[3],LEN[4]. (4 IDENTICAL HUMAN V-KAPPA-IV; ALSO 2 HUMAN V-KAPPA-I: V19B'CL[88], V18B'CL[89]; 1 MOUSE V-KAPPA-I: MCPC603[47]; 30 MOUSE V-KAPPA-III: MPC11'CL[6],TEPC111[7],PC3741(NZB)[8],TEPC124[9], MOPC321[12],PC7043(NZB)[13],PC7183(NZB)[14],PC6308(NZB)[15],PC6684(NZB)[17],PC7940(NZB)[18],PC7175(NZB)[19], PC2485(NZB)[20],PC4039(NZB)[21],PC7210(NZB)[23],H36-15[26],2242[29],V-21E1.5KB'CL[30],V-21C9.5KB'CL[31], PC7461(NZB)[33],PC2960(NZB)[34],97.C(A.BY)[35],10.A(A.TH)[39],H36-5[48],40.C(A.TH)[52],MOPC63[54],ABPC22[55], PC9245(NZB)[56],PC4050(NZB)[57],V-21B16KB'CL[58],11949[62]; 1 MOUSE V-KAPPA-VI: BFPC61A'CL[64]; AND 15 RABBIT V-KAPPA: K9-335-I[19],3368[20],BS-5[38],BS-1[39],K49-501[45],3547[47],K4820[57],K30-267[61],311[65],4422[66],17D9'CL[68], 4192[71],4363[85],120[103],K-25[112].)

FR3: SET 1: VJI'CL[1],VKAPPA IV GERMLINE'CL[2],PB17IV'CL[3],LEN[4]. (4 IDENTICAL)

FR4: SET 1: PB17IV'CL[3]. (IDENTICAL TO 3 HUMAN V-KAPPA-I: AU[2],GAL(I)[36],CL*[110]; 2 HUMAN V-KAPPA-II: GM 607 'CL[5], RPM1-6410'CL[16]; AND 7 HUMAN V-KAPPA-III: WOL[2],PAY[7],PIE[11],GLO[15],CUR[20],REE[57],VKAPPA3'CL[82].)
SET 2: LEN[4]. (IDENTICAL TO 3 HUMAN V-KAPPA-I: AG[7],DEN[46],BI[63]; 2 HUMAN V-KAPPA-II: NIM[3],FR[14]; AND 6 HUMAN V-KAPPA-III: NEU[5],GOT[6],GAR'[10],FLO[12],FR4[21],IARC/BL41'CL[28].)
SET 3: VJI'CL[1]. (IDENTICAL TO 1 HUMAN V-KAPPA-III: SON[8].)

IDENTICAL SETS OF COMPLEMENTARITY DETERMINING REGIONS:

CDR1: SET 1: VJI'CL[1],VKAPPA IV GERMLINE'CL[2]. (2 IDENTICAL)

CDR2: SET 1: VJI'CL[1],VKAPPA IV GERMLINE'CL[2],PB17IV'CL[3],LEN[4]. (4 IDENTICAL HUMAN V-KAPPA-IV; ALSO 1 MOUSE V-KAPPA-VI: KPNI6 'CL[70].)

CDR3:

IDENTICAL SETS OF J-MINIGENES:

SET 1: PB17IV'CL[3]. (IDENTICAL TO 1 HUMAN V-KAPPA-I: AU[2]; 1 HUMAN V-KAPPA-II: RPM1-6410'CL[16]; AND 2 HUMAN V-KAPPA-III: PIE[11],VKAPPA3'CL[82].)

+ THE FOLLOWING WERE EQUALLY AND MOST FREQUENTLY OCCURRING:

AT POSITION	RESIDUES
22	(SER,ASP,ASN)
96	(TRP,TYR)
104	(LEU,VAL)

HUMAN LAMBDA LIGHT CHAINS SUBGROUP I

		INVARIANT RESIDUES	1* NEWM	2 HA	3 LR	4 NIG -64	5 NEW	6 BL2 CL	7 WAH	8 NIG -77	9 VOR	10 RHE	11 LOC	12 OKA	13 AMYLOID EPS	14 HBJ 7	15 COX	16* KOH	17 HS 92	18 HS 78	19 NIG -51	20 HS 94	21 HBJ 11	22 BJ 98	23 MZ
	0		---	---	---	---	---	---	---	---	---	---	---	---		---	---	---	---	---	---	---	---		
	1	PCA(.95)	PCA	PCA	PCA	PCA	PCA	gln	PCA	PCA	PCA	PCA	PCA	PCA		PCA	PCA	PCA	PCA	PCA	PCA	PCA	PCA		
	2	SER	SER	SER	SER	SER	SER	SER	SER	SER	SER	SER	SER	SER		SER	SER	SER	SER	SER	SER	SER	SER		
	3	VAL(.95)	VAL	VAL	VAL	VAL	VAL	VAL	VAL	VAL	VAL	VAL	VAL	VAL	VAL	VAL	VAL	VAL	VAL	ala	VAL	VAL	VAL		
	4	LEU	LEU	LEU	LEU	LEU	LEU	LEU	LEU	LEU	LEU	LEU	LEU	LEU	LEU	LEU	LEU	LEU	LEU	LEU	LEU	LEU	LEU		
	5	THR	THR	THR	THR	THR	THR	THR	THR	THR	THR	THR	THR	THR	THR	THR	THR	THR	THR	THR	THR	THR	THR	THR	
	6	GLN(.95)	GLN	GLN	GLN	GLN	GLN	GLN	GLN	GLN	GLN	GLN	GLN	GLN	GLN	GLN	GLN	GLX	GLN	GLN	GLN	GLN	GLN		
	7	PRO	PRO	PRO	PRO	PRO	PRO	PRO	PRO	PRO	PRO	PRO	PRO	PRO	PRO	PRO	PRO	PRO	PRO	PRO	PRO	PRO	PRO		
	8	PRO	PRO	PRO	PRO	PRO	PRO	PRO	PRO	PRO	PRO	PRO	PRO	PRO	PRO	PRO	PRO	PRO	PRO	PRO	PRO	PRO	PRO		
	9	SER	SER	SER	SER	SER	SER	SER	SER	SER	SER	SER	SER	SER	SER	SER	SER	SER	SER	SER	SER	SER	SER		
	10		---	---	---	---	---	---	---	---	---	---	---	---	---	---	---	---	---	---	---	---	---		
FR1	11		VAL	VAL	VAL	VAL	VAL	VAL	ala	ala	ala	ala	ala	ala	leu	ala	ala	ala	VAL	VAL	ala	VAL	ala		
	12	SER	SER	SER	SER	SER	SER	SER	SER	SER	SER	SER	SER	SER	SER	SER	SER	SER	SER	SER	SER	SER	SER	SER	
	13		GLY	GLY	GLY	ala	ala	ala	GLY	GLY	GLY	GLY	GLY	GLY	ala	GLY	GLY	GLY	GLY	GLY	GLY	ala	GLY	ala	
	14		ALA	thr	ALA	ALA	ALA	ALA	thr	thr	thr	thr	thr	thr	ALA	thr	thr	thr	ALA	ALA	val	ALA	thr	ALA	
	15	PRO(.95)	PRO	PRO	PRO	PRO	PRO	PRO	PRO	PRO	PRO	PRO	PRO	PRO	PRO	PRO	ser	PRO	PRO	PRO	PRO	PRO	PRO		
	16	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY		
	17		GLN	GLN	glu	GLN	GLN	GLN	GLN	GLN	GLN	GLN	GLN	GLN	GLN	GLN	GLN	GLX	GLN	GLN	GLN	GLN	GLN		
	18		ARG	ARG	ARG	glu	lys	lys	ARG	ARG	ARG	ARG	ARG	ARG	ARG	gly	ARG	ser	ARG	thr	ser	ARG	ARG		
	19	VAL(.95)	VAL	VAL	VAL	VAL	VAL	VAL	VAL	VAL	VAL	VAL	VAL	VAL	VAL	VAL	VAL	VAL		VAL	VAL			VAL	ala
	20		THR	THR	glu	THR	THR	THR	THR	THR	THR	THR	THR	THR	ser	THR	THR	THR		THR	ile			THR	ile
	21	ILE(.95)	ILE	ILE	ILE	ILE	ILE	ILE	ILE	ILE	ILE	ILE	ILE	ILE	ILE	ILE	ILE	ILE			ILE			ser	ILE
	22	SER(.95)	SER	SER	SER	SER	SER	SER	SER	SER	SER	SER	SER	SER	SER	SER	SER	SER			SER			ile	SER
	23	CYS	CYS	CYS	CYS	CYS	CYS	CYS	CYS	CYS	CYS	CYS	CYS	CYS	CYS	CYS	CYS				CYS			CYS	CYS
	24		THR	SER	SER	SER	SER	SER	PHE	SER	SER	THR	SER	SER	SER	SER	SER				SER				SER
	25	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY				GLY				GLY
	26		SER	GLY		SER	GLY	SER	SER	SER	GLY	SER	SER	SER	SER	SER	SER				SER				SER
	27		SER	SER		SER	SER	SER	SER	THR	ASN	ALA	SER	GLY	SER		SER				SER				SER
	27A		---	---		---	---	---	---	---	---	---	---	---	---		---				---				---
	27B		---	---		---	---	---	---	---	---	---	---	---	---		---				---				---
	27C		---	---		---	---	---	---	---	---	---	---	---	---		---				---				---
CDR1	27D		SER	SER		SER	THR	SER	SER	SER	PHE	THR	SER	SER	---		SER				SER				SER
	27E		ASN	ASN		ASN	ASN	ASN	ASN	ASN	ASP	ASP	ASN	ASN	SER		ASN				ASN				ASN
	27F		ILE	GLY		---	---	---	---	---	---	---	ILE	---	ASN		---				---				---
	28		GLY	THR		ILE	ILE	ILE	ILE	ILE	ILE	ILE	GLY	ILE	ILE		LEU				ILE				MET
	29		ALA	GLY		GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLU	GLY	GLY		GLY				GLY				
	30		GLY	ASN		ASP	ASN	ASN	ARG	SER	ARG	SER	THR	SER	LYS		SER				ARG				
	31		ASN	ASN		ASN	ASN	ASP	TYR	ASN	ASN	ASN	ASN	HIS	ASN		ASN				ASN				
	32		HIS	TYR		PHE	TYR	TYR	TYR	THR	SER	SER	SER	THR	TYR		GLN				THR				
	33	VAL	VAL	VAL		VAL	VAL	VAL	VAL	VAL	VAL	VAL	VAL	VAL	VAL		VAL				VAL				
	34		LYS	TYR		SER	SER	SER	TYR	THR	ASN	ILE	SER	ASN	ASP		ASN				ASN				
	35	TRP	TRP	TRP		TRP	TRP	TRP	TRP	TRP	TRP	TRP	TRP	TRP	TRP		TRP				TRP				
	36		TYR	TYR		TYR	HIS	TYR	TYR	TYR	TYR	TYR	TYR	TYR	TYR		TYR				TYR				
	37		GLN	GLN		GLN	GLN	GLN	GLN	GLN	GLN	GLN	GLN	HIS	GLN		ARG				GLN				
	38		GLN	GLN		GLN	HIS	GLN	GLN	HIS	VAL	GLN	HIS	GLN	GLN		HIS				GLN				
	39		LEU	LEU		LEU	LEU	VAL	LEU	LEU	HIS	VAL	LEU	PHE	LEU		LEU				VAL				
	40	PRO	PRO	PRO		PRO	PRO	PRO	PRO	PRO	PRO	PRO	PRO	PRO	PRO		PRO				PRO				
FR2	41	GLY	GLY	GLY		GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY		GLY				GLY				
	42		THR	THR		THR	THR	THR	THR	THR	THR	LYS	THR	THR	THR		THR				ALA				
	43		ALA	ALA		ALA	ALA	ALA	THR	ALA	ALA	ALA	ALA	ALA	ALA		ALA				ALA				
	44	PRO	PRO	PRO		PRO	PRO	PRO	PRO	PRO	PRO	PRO	PRO	PRO	PRO		PRO				PRO				
	45		LYS	LYS		LYS	LYS	LYS	LYS	LYS	ARG	LYS	LYS	LYS	LYS		LYS				LYS				
	46	LEU	LEU	LEU		LEU	LEU	LEU	LEU	LEU	LEU	LEU	LEU	LEU	LEU		LEU				LEU				
	47		LEU	LEU		LEU	LEU	LEU	LEU	LEU	LEU	LEU	LEU	LEU	LEU		VAL				LEU				
	48		ILE	ILE		ILE	ILE	ILE	ILE	ILE	ILE	ILE	ILE	ILE	ILE		ILE				VAL				
	49		PHE	TYR		TYR	TYR	TYR	TYR	TYR	TYR	TYR	TYR	TYR	PHE		TYR				TYR				
	50		HIS	ARG		ASP	GLU	ASP	LYS	SER	SER	TYR	GLU	ARG	ASN		SER				SER				
	51		ASN	ASP		ASN	ASP	ASN	ASP	ASN	SER	ASN	ASP	ASN	ASN		ASP				ASN				
CDR2	52		ASN	ASP		ASN	ASN	ASN	ASN	ASP	ASP	ASP	ASN	ASP	ASN		SER				ASN				
	53		ALA	LYS		LYS	LYS	LYS	GLN	GLN	GLN	LEU	SER	GLN	LYS		GLN				GLN				
	54		ARG	ARG		ARG	ARG	ARG	ARG	ARG	ARG	LEU	ARG	ARG	ARG		ARG				TRP				
	55		---	PRO		PRO	PRO	PRO	PRO	PRO	SER	PRO	ALA	PRO			PRO				PRO				
	56	SER	---	SER		SER	SER	SER	SER	SER	SER	SER	SER	SER			SER				SER				
	57	GLY	---	GLY		GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY			GLY				GLY				
	58		---	VAL		ILE	ILE	ILE	VAL	VAL	VAL	VAL	VAL	VAL			VAL				VAL				
	59		---	PRO		PRO	PRO	PRO	PRO	PRO	PRO	SER	SER	PRO			PRO				PRO				
	60		---	ASP		ASP	ASP	ASP	ASP	HIS	ASP	ASP	ASP	ASP			ASP				ASP				
	61	ARG	---	ARG		ARG	ARG	ARG	ARG	ARG	ARG	ARG	ARG	ARG	ARG		ARG				ARG				
	62		PHE	PHE		PHE	ILE	PHE	PHE	PHE	PHE	PHE	PHE	PHE	PHE		ILE				PHE				
	63	SER	SER	SER		SER	SER	SER	SER	SER	SER	SER	SER	SER	SER		SER				SER				
	64		VAL	GLY		GLY	ALA	GLY	GLY	GLY	GLY	ALA	ALA	GLY	GLY		ALA				GLY				
	65	SER	SER	SER		SER	SER	SER	SER	SER	SER	SER	SER	SER	SER		SER				SER				
	66	LYS	LYS	LYS		LYS	LYS	LYS	LYS	LYS	LYS	LYS	LYS	LYS	LYS		LYS				LYS				
	67	SER	SER	SER		SER	SER	SER	SER	SER	SER	SER	SER	SER	SER		SER				SER				
	68	GLY	GLY	GLY		GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY		GLY				GLY				
	69		SER	THR		THR	THR	THR	THR	ALA	THR	THR	THR	THR	THR		THR				THR				
	70	SER	SER	SER		SER	SER	SER	SER	SER	SER	SER	SER	SER	SER		SER				SER				
FR3	71	ALA	ALA	ALA		ALA	ALA	ALA	ALA	ALA	ALA	ALA	ALA	ALA	ALA		ALA				ALA				
	72	THR	SER	THR		THR	THR	THR	SER	SER	SER	SER	SER	SER	THR		SER				SER				
	73	LEU	LEU	LEU		LEU	LEU	LEU	LEU	LEU	LEU	LEU	LEU	LEU	LEU		LEU				LEU				
	74		ALA	ALA		GLY	ALA	GLY	ALA	ALA	ALA	ALA	ALA	ALA	GLY		ALA				ALA				
	75	ILE	ILE	ILE		ILE	ILE	ILE	ILE	ILE	ILE	ILE	ILE	ILE	ILE		ILE				ILE				
	76		THR	SER		THR	THR	THR	SER	SER	SER	SER	SER	SER	THR		SER				SER				
	77	GLY	GLY	GLY		GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY		GLY				GLY				
	78	LEU	LEU	LEU		LEU	LEU	LEU	LEU	LEU	LEU	LEU	LEU	LEU	LEU		LEU				LEU				
	79		GLN	ARG		GLN	ARG	GLN	ARG	GLN	GLN	GLU	GLN	GLN	GLN		GLN				HIS				
	80		ALA	SER		THR	THR	THR	SER	SER	SER	SER	PRO	SER	THR		SER				SER				
	81		GLU	GLU		GLY	GLY	GLY	GLU	GLU	GLU	GLU	GLU	GLU	GLY		GLU				GLU				
	82		ASP	ASP		ASP	ASP	ASP	ASP	ASP	ASN	ASP	ASP	ASP	ASP		ASP				ASP				
	83	GLU	GLU	GLU		GLU	GLU	GLU	GLU	GLU	GLU	GLU	GLU	GLU	GLU		GLU				GLU				
	84		ALA	ALA		ALA	ALA	ALA	ALA	THR	ALA	ALA	THR	ALA	ALA		SER				ALA				
	85		ASP	HIS		ASP	ASP	ASP	ASP	ASP	ASP	ASP	ASP	ASP	ILE		ASP				ASP				
	86	TYR	TYR	TYR		TYR	TYR	TYR	TYR	TYR	TYR	TYR	TYR	TYR	TYR		TYR				TYR				
	87		TYR	HIS		TYR	TYR	TYR	TYR	TYR	PHE	TYR	TYR	TYR	TYR		TYR				PHE				
	88	CYS	CYS	CYS		CYS	CYS	CYS	CYS	CYS	CYS	CYS	CYS	CYS	CYS		CYS				CYS				
	89		GLN	ALA		GLY	ALA	GLY	ALA	ALA	ALA	ALA	ALA	ALA	GLY		ALA				ALA				
	90		SER	ALA		THR	THR	THR	ALA	THR	THR	ALA	ALA	ALA	THR		SER				THR				
	91		TYR	TRP		TRP	TRP	TRP	TRP	TRP	TRP	TRP	TRP	TRP	TYR		TRP				TRP				
	92		ASP	ASP		ASP	ASP	ASN	ASP	ASP	ASP	ASN	ASP	ASP	ASP		ASP				ASP				
	93		ARG	TYR		SER	SER	ASN	ASP	ASP	ASP	ASP	ASP	ASP	ASN		ASP				ASP				
	94		SER	ARG		SER	SER	SER	SER	SER	SER	SER	SER	SER	ARG		SER				SER				
CDR3	95		LEU	LEU		LEU	LEU	LEU	LEU	LEU	LEU	LEU	LEU	LEU	ARG		LEU				LEU				
	95A		---	SER		SER	ASN	SER	---	ASN	ASP	ASP	ASP	ASP	---		ASP				ASP				
	95B		---	ALA		VAL	ALA	GLY	---	GLY	GLY	GLU	VAL	GLY	---		GLY				GLY				
	95C		---	---		---	---	---	---	---	---	---	---	---	---		---				---				
	95D		---	---		---	---	---	---	---	---	---	---	---	---		---				---				
	95E		---	---		---	---	---	---	---	---	---	---	---	---		---				---				
	95F		---	---		---	---	---	---	---	---	---	---	---	---		---				---				
	96		ARG	VAL		GLY	VAL	TRP	TRP	PRO	PRO	PRO	ALA	PRO	SER		PRO				PRO				
	97		VAL	VAL		MET	VAL	VAL	VAL	VAL	VAL	GLY	VAL	VAL	VAL		VAL				VAL				
	98	PHE	PHE	PHE		PHE	PHE	PHE	PHE	PHE	PHE	PHE	PHE	PHE	PHE		PHE				PHE				
	99	GLY	GLY	GLY		GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY		GLY				GLY				
	100		GLY	GLY		GLY	GLY	GLY	GLY	GLY	GLY	GLY	THR	GLY	GLY		GLY				GLY				
	101	GLY	GLY	GLY		GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY		GLY				GLY				
FR4	102	THR	THR	THR		THR	THR	THR	THR	THR	THR	THR	THR	THR	THR		THR				THR				
	103		LYS	GLN		ARG	LYS	LYS	THR	LYS	LYS	LYS	LYS	LYS	ASN		LYS				LYS				
	104		LEU	LEU		VAL	VAL	LEU	LEU	VAL	VAL	LEU	VAL	LEU	VAL		VAL				LEU				
	105	THR	THR	THR		THR	THR	THR	THR	THR	THR	THR	THR	THR	THR		THR				THR				
	106	VAL	VAL	VAL		VAL	VAL	VAL	VAL	VAL	VAL	VAL	VAL	VAL	VAL		VAL				VAL				
	106A		LEU	LEU		LEU	LEU	LEU	LEU	GLN	LEU	LEU	LEU	LEU	VAL		LEU				LEU				
	107		ARG	ARG		GLY	GLY	GLY	SER	GLY	GLY	GLY	GLY	GLY	GLY		GLY				GLY				
	108	GLN	GLN	GLN			GLN		GLN	GLN	GLN	GLN	GLN	GLN	GLN		GLN				GLN				
	109	PRO	PRO	PRO			PRO		PRO	PRO	PRO	PRO	PRO	PRO	PRO		PRO				PRO				

HUMAN LAMBDA LIGHT CHAINS SUBGROUP I (cont'd)

		24 FUL #	# OF SEQUENCES	# OF AMINO ACIDS	OCCURRENCES OF MOST COMMON AMINO ACID	VARIABILITY
	0					
	1		20	2	19(PCA)	2.1
	2		20	1	20(SER)	1.
	3		21	2	20(VAL)	2.1
	4		21	1	21(LEU)	1.
	5		22	1	22(THR)	1.
	6		21	1 : 2	21(GLN) : 20(GLN)	1. : 2.1
	7		21	1	21(PRO)	1.
	8		21	1	21(PRO)	1.
	9		21	1	21(SER)	1.
	10					
FR1	11		21	3	11(ALA)	5.7
	12		22	1	22(SER)	1.
	13		22	2	16(GLY)	2.8
	14		22	3	11(THR)	6.
	15		21	2	20(PRO)	2.1
	16		21	1	21(GLY)	1.
	17		21	2	20(GLN) : 19(GLN)	2.1 : 2.2
	18		21	6	14(ARG)	9.
	19		20	2	19(VAL)	2.1
	20		20	4	16(THR)	5.
	21		19	2	18(ILE)	2.1
	22		19	2	18(SER)	2.1
	23	CYS	19	1	19(CYS)	1.
	24	SER	18	3	15(SER)	3.6
	25	GLY	18	1	18(GLY)	1.
	26	ASN	17	3	13(SER)	3.9
	27	SER	16	5	12(SER)	6.7
	27A	---				
	27B	---				
	27C	---				
CDR1	27D	SER	15	3	12(SER)	
	27E		15	3	12(ASN)	
	27F		4	3	2(ILE)	
	28		15	5	10(ILE)	7.5
	29		14	3	12(GLY)	3.5
	30		14	7	4(SER)	25.
	31		14	4	11(ASN)	5.1
	32		14	6	5(TYR)	17.
	33		14	1	14(VAL)	1.
	34		14	7	4(+)	25.
	35		14	1	14(TRP)	1.
	36		14	2	13(TYR)	2.2
	37		14	3	12(GLN)	3.5
	38		14	3	9(GLN)	4.7
	39		14	4	9(LEU)	6.2
	40		14	1	14(PRO)	1.
	41		14	1	14(GLY)	1.
FR2	42		14	3	12(THR)	3.5
	43		14	2	13(ALA)	2.2
	44		14	1	14(PRO)	1.
	45		14	2	13(LYS)	2.2
	46		14	1	14(LEU)	1.
	47		14	2	13(LEU)	2.2
	48		14	2	13(ILE)	2.2
	49		14	2	12(TYR)	2.3
	50		14	8	4(SER)	28.
	51		14	3	8(ASN)	5.3
CDR2	52		14	3	8(ASN)	5.3
	53		14	5	6(GLN)	12.
	54		14	3	12(ARG)	3.5
	55		12	3	10(PRO)	3.6
	56		12	1	12(SER)	1.
	57		12	1	12(GLY)	1.
	58		12	2	9(VAL)	2.7
	59		12	2	10(PRO)	2.4
	60		12	2	11(ASP)	2.2
	61		13	1	13(ARG)	1.
	62		14	2	12(PHE)	2.3
	63		14	1	14(SER)	1.
	64		14	3	9(GLY)	4.7
	65		14	1	14(SER)	1.
	66		14	1	14(LYS)	1.
	67		14	1	14(SER)	1.
	68		14	1	14(GLY)	1.
	69		14	3	12(THR)	3.5
	70		14	1	14(SER)	1.
	71		14	1	14(ALA)	1.
FR3	72		14	2	9(SER)	3.1
	73		14	1	14(LEU)	1.
	74		14	2	11(ALA)	2.5
	75		14	1	14(ILE)	1.
	76		14	2	9(SER)	3.1
	77		14	1	14(GLY)	1.
	78		14	1	14(LEU)	1.
	79		14	4	9(GLN)	6.2
	80		14	4	8(SER)	7.
	81		14	2	10(GLU)	2.8
	82		14	2	13(ASP)	2.2
	83		14	1	14(GLU)	1.
	84		14	3	11(ALA)	3.8
	85		14	3	12(ASP)	3.5
	86		14	1	14(TYR)	1.
	87		14	3	11(TYR)	3.8
	88		14	1	14(CYS)	1.
	89		14	3	10(ALA)	4.2
	90		14	3	7(THR)	6.
	91		14	2	12(TRP)	2.3
	92		14	2	12(ASP)	2.3
	93		14	5	8(ASP)	8.8
	94		14	2	12(SER)	2.3
	95		14	2	13(LEU)	2.2
	95A		11	3	6(ASP)	
CDR3	95B		11	4	6(GLY)	
	95C					
	95D					
	95E					
	95F					
	96		14	7	6(PRO)	16.
	97		14	3	12(VAL)	3.5
	98		14	1	14(PHE)	1.
	99		14	1	14(GLY)	1.
	100		14	2	13(GLY)	2.2
	101		14	1	14(GLY)	1.
	102		14	1	14(THR)	1.
FR4	103		14	5	10(LYS)	7.
	104		14	2	7(+)	4.
	105		14	1	14(THR)	1.
	106		14	1	14(VAL)	1.
	106A		14	3	12(LEU)	
	107		14	3	11(GLY)	3.8
	108		12	1	12(GLN)	1.
	109		12	1	12(PRO)	1.

ANTIBODY SPECIFICITIES: HUMAN LAMBDA LIGHT CHAINS SUBGROUP I

1) **NEWM:** ANTI-3-(3'-HYDROXY-3',7',11',15'-TETRAMETHYL HEXADECYL) 2-METHYL 1,4 NAPHTHOQUINONE(VIT.K1OH)
16) **KOH:** ANTI-HUMAN GAMMA G GLOBULIN

REFERENCE: HUMAN LAMBDA LIGHT CHAINS SUBGROUP I

1) **NEWM:** CHEN,B.L. & POLJAK,R.J. (1974) BIOCHEMISTRY,13,1295-1302. (CHECKED BY AUTHOR 01/24/78)
2) **HA:** SHINODA,T.,TITANI,K. & PUTNAM,F.W. (1970) J.BIOL.CHEM.,245,4475-4487. (CHECKED BY AUTHOR 06/15/83)
3) **LR:** CAULIN-GLASER,T.,PRELLI,F. & FRANKLIN,E.C. (1982) J.LAB.CLIN.MED.,99,845-851. (CHECKED BY AUTHOR 12/10/82)
4) **NIG-64:** TONOIKE,H.,KAMETANI,F.,HOSHI,A.,SHINODA,T. & ISOBE,T. (1985) BIOCHEM.BIOPHYS.RES.COMMUN.,126,1228-1234.
5) **NEW:** LANGER,B.,STEINMETZ-KAYNE,M. & HILSCHMANN,N. (1968) Z.PHYSIOL.CHEM.,349,945-951.
6) **BL2 'CL:** TSUJIMOTO,Y. & CROCE,C.M. (1984) NUC.ACIDS RES.,12,8407-8414.
7) **WAH:** TAKAHASHI,Y.,TAKAHASHI,N.,TETAERT,D. & PUTNAM,F.W. (1983) PROC.NAT.ACAD.SCI.USA,80,3686-3690. (CHECKED BY AUTHOR 06/15/83)
8) **NIG-77:** TONOIKE,H.,KAMETANI,F.,HOSHI,A.,SHINODA,T. & ISOBE,T. (1985) BIOCHEM.BIOPHYS.RES.COMMUN.,126,1228-1234.
9) **VOR:** ENGELHARD,M.,HESS,M. & HILSCHMANN,N. (1974) Z.PHYSIOL.CHEM.,355,85-88; ENGELHARD,M. & HILSCHMANN,N. (1975) Z.PHYSIOL.CHEM.,356, 1413-1444.
10) **RHE:** FUREY,W. JR.,WANG,B.C.,YOO,C.S. & SAX,M. (1983) J.MOL.BIOL.,167,661-692. (CHECKED BY AUTHOR 05/15/84)
11) **LOC:** ZHU,D.,KIM,H.S. & DEUTSCH,H.F. (1983) MOL.IMMUNOL.,20,1107-1116.
12) **OKA:** ZHU,D.,KIM,H.S. & DEUTSCH,H.F. (1983) MOL.IMMUNOL.,20,1107-1116.
13) **AMYLOID EPS:** TOFT,K.G.,SLETTEN,K. & HUSBY,G. (1985) BIOL.CHEM.HOPPE-SEYLER,366,617-625.
14) **HBJ7:** HOOD,L.,GRAY,W.R.,SANDERS,B.G. & DREYER,W.J. (1967) COLD SPRING HARBOR SYMP. QUANTITATIVE BIOL.,32,133-145.
15) **COX:** ZHU,D.,KIM,H.S. & DEUTSCH,H.F. (1983) MOL.IMMUNOL.,20,1107-1116.
16) **KOH:** KAPLAN,A.P. & METZGER,H. (1969) BIOCHEMISTRY,8,3944-3951.
17) **HS92:** HOOD,L. & EIN,D. (1968) NATURE,220,764-767; (1968) SCIENCE,1662,679-681.
18) **HS78:** HOOD,L. & EIN,D. (1968) NATURE,220,764-767; (1968) SCIENCE,1662,679-681.
19) **NIG-51:** TAKAHASHI,N.,TAKAYASU,T.,SHINODA,T.,ITO,S.,OKUYAMA,T. & SHIMIZU,A. (1980) BIOMED.RES.,1,321-333. (CHECKED BY AUTHOR 01/28/81)
20) **HS94:** HOOD,L. & EIN,D. (1968) NATURE,220,764-767; (1968) SCIENCE,1662,679-681.
21) **HBJ11:** HOOD,L.,GRAY,W.R.,SANDERS,B.G. & DREYER,W.J. (1967) COLD SPRING HARBOR SYMP. QUANTITATIVE BIOL.,32,133-145.
22) **BJ98:** BAGLIONI,C. (1967) BIOCHEM.BIOPHYS.RES.COMMUN.,26,82-89.
23) **MZ:** MILSTEIN,C.,FRANGIONE,B. & PINK,J.R.L. (1967) COLD SPRING HARBOR SYMP. QUANTITATIVE BIOL.,32,31-36. (CHECKED BY AUTHOR 10/17/77)
24) **FUL:** SOX,H.C.,JR. & HOOD,L. (1970) PROC.NAT.ACAD.SCI.USA,66,975-982.

NOTES: HUMAN LAMBDA LIGHT CHAINS SUBGROUP I

IDENTICAL SETS OF FRAMEWORK SEGMENTS:

FR1: SET 1: WAH[7],NIG-77[8],VOR[9],RHE[10],LOC[11],OKA[12]. (6 IDENTICAL)

FR2: SET 1: NEWM[1],AMYLOID EPS[13]. (2 IDENTICAL)
SET 2: HA[2],NIG-64[4]. (2 IDENTICAL)
SET 3: NIG-77[8],LOC[11]. (2 IDENTICAL)

FR3: SET 1: NIG-64[4],BL2 'CL[6]. (2 IDENTICAL)

FR4: SET 1: NEWM[1]. (IDENTICAL TO 1 HUMAN V-LAMBDA-II: WH[3]; AND 1 HUMAN V-LAMBDA-V: BO[1].)
SET 2: NEW[5],VOR[9],COX[15]. (3 IDENTICAL HUMAN V-LAMBDA-I; ALSO 1 HUMAN V-LAMBDA-VI: AMYLOID-AR[1]; AND 6 MOUSE V-LAMBDA: MOPC315[25],TEPC952[26],MA8-13[27],5-7[29],MOPC315-26'CL'[30],MOPC315-37'CL[32].)
SET 3: BL2 'CL[6],RHE[10],OKA[12],NIG-51[19]. (4 IDENTICAL HUMAN V-LAMBDA-I; ALSO 5 HUMAN V-LAMBDA-II: MES[2],ES492[8],TRO[14], VIL[17],WIN[21]; 4 HUMAN V-LAMBDA-III: HIL[1],CAP[4],BAU[12],DEL[14]; 1 HUMAN V-LAMBDA-IV: SH[1]; 3 HUMAN V-LAMBDA-VI: SUT[2],THO[4],LBV'CL[5]; AND 24 MOUSE V-LAMBDA: MOPC104E[1],J558[2],XS104[3],HOPC1[4],J698[5],H2061[6],W3159[7], Y5431[8],Y5485[9],Y5830[10],Y5669[11],MOPC511(L)[12],S178[13],Y5444[14],Y5606[15],S176[16],H2020[17],RPC20[18],IG 303LAMBDA'CL[19],S43'CL[21],S2H5'CL[38],S2E9'CL[39],S1F12'CL[40],IG 25LAMBDA'CL[41].)
SET 4: LOC[11]. (IDENTICAL TO 1 HUMAN V-LAMBDA-V: MCG[3].)

IDENTICAL SETS OF COMPLEMENTARITY DETERMINING REGIONS:

CDR1:

CDR2: SET 1: NIG-64[4],BL2 'CL[6]. (2 IDENTICAL)

CDR3: SET 1: VOR[9],NIG-51[19]. (2 IDENTICAL)

IDENTICAL SETS OF J-MINIGENES:

SET 1: NEW[5]. (IDENTICAL TO 1 HUMAN V-LAMBDA-VI: AMYLOID-AR[1].)
SET 2: BL2 'CL[6]. (IDENTICAL TO 2 HUMAN V-LAMBDA-VI: SUT[2],THO[4]; AND 24 MOUSE V-LAMBDA: MOPC104E[1],J558[2],XS104[3],HOPC1[4], J698[5],H2061[6],W3159[7],Y5431[8],Y5485[9],Y5830[10],Y5669[11],MOPC511(L)[12],S178[13],Y5444[14],Y5606[15],S176[16], H2020[17],RPC20[18],IG 303LAMBDA'CL[19],S43'CL[21],S2H5'CL[38],S2E9'CL[39],S1F12'CL[40],IG 25LAMBDA'CL[41].)
SET 3: VOR[9],COX[15]. (2 IDENTICAL)
SET 4: OKA[12],NIG-51[19]. (2 IDENTICAL)

SPECIFIC NOTES:

24) **FUL:** SOX AND HOOD HAVE REPORTED FOUR HUMAN V KAPPA AND ONE V LAMBDA CHAINS WITH ASN-SER/THR TO CONTAIN CARBOHYHDRATE.

+ THE FOLLOWING WERE EQUALLY AND MOST FREQUENTLY OCCURRING:

AT POSITION	RESIDUES
34	(SER,ASN)
104	(LEU,VAL)

HUMAN LAMBDA LIGHT CHAINS SUBGROUP II

		INVARIANT RESIDUES	1 NIG -84	2 MES	3 WH	4 NEI	5 KAR	6 RIM	7 SLA	8 ES492	9 WEIR	10 TOG	11 SM #	12 HS 68	13 HS 77	14 TRO	15 BOH	16 NIG -58	17 VIL	18 HBJ 15	19 HBJ 8	20 HS 70	21 WIN	22 BUR	23 PRE	24 HS 86
	0		---	---	---	---	---	---	---	---	---	---	---	---	---	---	---	---	---	---	---	---	---	---	---	---
	1		PCA	PCA	PCA	PCA	PCA	PCA	PCA	PCA	PCA	PCA	PCA	PCA	PCA	PCA	PCA	PCA	his	PCA	PCA	PCA	PCA	PCA	PCA	PCA
	2	SER(.96)	SER	SER	SER	SER	SER	SER	SER	SER	SER	SER	SER	SER	SER	SER	SER	SER	SER	SER	SER	SER	SER	SER	SER	SER
	3		ALA	ALA	ALA	ALA	ALA	ALA	ALA	ALA	ALA	ALA	ALA	ALA	ALA	ALA	ALA	ALA	ALA	ALA	ALA	ALA	ALA	ALA	ALA	pro
	4	LEU(.96)	LEU	LEU	LEU	LEU	LEU	LEU	LEU	LEU	LEU	LEU	LEU	LEU	LEU	LEU	LEU	LEU	LEU	LEU	LEU	LEU	LEU	LEU	LEU	LEU
	5		THR	THR	THR	THR	THR	THR	THR	THR	THR	THR	THR	THR	THR	THR	THR	THR	THR	ala	ser	THR	THR	THR	THR	ala
	6	GLN(.96)	GLN	GLN	GLN	GLN	GLN	GLN	GLN	GLN	GLN	GLN	GLN	GLN	GLN	GLN	GLN	GLN	GLN	GLN	GLN	GLN	GLX	GLN	GLX	GLN
	7		PRO	PRO	PRO	PRO	PRO	PRO	PRO	PRO	PRO	PRO	PRO	PRO	PRO	PRO	PRO	PRO	PRO	PRO	PRO	PRO	PRO	ser	PRO	ALA
	8		ALA	ALA	ALA	ALA	ALA	ALA	ALA	ALA	ALA	ALA	ALA	ALA	ALA	arg	arg	arg	ALA	ALA	ALA	pro	arg	pro	ALA	SER
	9	SER(.96)	SER	SER	SER	SER	SER	SER	SER	SER	SER	SER	SER	SER	SER	SER	SER	SER	SER	SER	SER	arg	SER	SER	SER	SER
FR1	10		---	---	---	---	---	---	---	---	---	---	---	---	---	---	---	---	---	---	---	---	---	---	---	---
	11		VAL	VAL	VAL	VAL	VAL	VAL	VAL	VAL	VAL	VAL	VAL	VAL	VAL	VAL	VAL	VAL	VAL	VAL	VAL	VAL	VAL	ala	VAL	SER
	12	SER(.96)	SER	SER	SER	SER	SER	SER	SER	SER	SER	SER	SER	SER	SER	SER	SER	SER	SER	SER	SER	SER	SER	SER	SER	GLY
	13		GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	ala	glu	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	SER
	14	SER(.96)	SER	SER	SER	SER	SER	SER	SER	SER	SER	SER	SER	SER	SER	SER	SER	SER	SER	SER	SER	SER	SER	SER	SER	SER
	15	PRO(.96)	PRO	PRO	PRO	PRO	PRO	PRO	PRO	PRO	PRO	PRO	PRO	PRO	PRO	PRO	PRO	PRO	leu	PRO	PRO	PRO	PRO	PRO	PRO	PRO
	16	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY
	17		GLN	GLN	GLN	GLN	GLN	GLN	GLN	GLN	GLN	GLN	GLN	GLN	GLN	GLN	GLN	GLN	GLN	GLN	GLN	GLN	GLN	his	GLN	glu
	18		SER	SER	SER	SER	SER	SER	SER	SER	SER	SER	SER	SER	SER	SER	SER	SER	thr	SER	SER	SER	SER	SER	SER	SER
	19		ILE	ILE	ILE	ILE	ILE	ILE	ILE	ILE	ILE	ILE	ILE	ILE	ILE	val	val	leu	ILE	ILE	ILE	val	val	val	ILE	ILE
	20	THR	THR	THR	THR	THR	THR	THR	THR	THR	THR	THR	THR	THR	THR	THR	THR	THR	THR	THR	THR	THR	THR	THR	THR	THR
	21		ILE	ILE	ILE	ILE	ILE	ILE	ILE	ILE	val	ILE	ILE			ILE	ILE	ILE	ILE				ILE	ILE	ILE	
	22		SER	SER	SER	SER	SER	SER	SER		SER	SER	SER			SER	SER	SER	SER				SER	SER	SER	
	23	CYS	CYS	CYS	CYS	CYS	CYS	CYS	CYS		CYS	CYS	CYS			CYS	CYS	CYS	CYS				CYS	CYS	CYS	
	24		THR	THR	THR	THR				ALA	ALA	THR	THR			THR	ALA	SER	THR				THR	ILE		
	25		GLY	GLY	GLY	GLY				GLY	GLY	GLY	GLY			GLY	GLY	GLY	GLY				GLY	GLY		
	26		THR	THR	THR	THR				THR	HIS	THR	ASX			THR	THR	ALA	THR				SER	THR		
	27		THR	SER	SER	THR				HIS	THR	THR	SER			SER	SER	PRO	SER				TYR	SER		
	27A		---	---	---	---				---	---	---	---			---	---	---	---				---	---		
	27B		---	---	---	---				---	---	---	---			---	---	---	---				---	---		
CDR1	27C		---	---	---	---				---	---	---	---			---	---	---	---				---	---		
	27D		SER	SER	SER	SER				SER	SER	ASN	SER			SER	SER	CYS	SER				SER	SER		
	27E		ASP	ASP	ASP	ASP				ASP	ASP	ASP	VAL			ASP	ASP	ASP	ASP				ASN	ASN		
	27F		VAL	VAL	VAL	VAL				VAL	VAL	ILE	VAL			VAL	VAL	VAL	VAL				VAL	VAL		
	28		GLY	GLY	GLY	GLY				ASN	ALA	GLY	GLY			GLY	GLY	ASP	GLY				THR	GLY		
	29		GLY	GLY	SER	SER				PHE	ASP	SER	---			ALA	GLY	GLY	GLY				GLY	ASP		
	30		TYR	TYR	TYR	TYR				THR	SER	TYR	---			TYR	ASN	CYS	TYR				TYR	TYR		
	31		ASP	ASN	ASN	ASN				ASX	ASN	SER	---			ASN	HIS	GLU	ASN				ASN	LYS		
	32		PHE	TYR	PHE	PHE				ALA	SER	TYR	---			SER	PHE	SER	TYR				HIS	TYR		
	33		VAL	VAL	VAL	VAL					ILE	VAL	---			VAL	VAL	VAL	VAL				VAL	VAL		
	34		SER	SER	SER	SER					SER	SER	---			SER	SER	SER	SER				SER	SER		
	35	TRP	TRP	TRP	TRP	TRP					TRP	TRP	---			TRP	TRP	TRP	TRP				TRP	TRP		
	36		TYR	PHE	TYR	TYR					TYR	PHE	---			TYR	TYR	TYR	PHE				TYR	TYR		
	37		GLN	GLN	GLN	GLN					GLN	GLN	---			GLN	GLN	GLN	GLN				GLN	GLX		
	38		GLN	GLN	GLN	GLN					LEU	GLN	---			GLN	GLN	GLN	GLN				GLN	GLX		
	39		HIS	HIS	HIS	ASN					HIS	HIS	---			HIS	HIS	HIS	HIS				ASP	HIS		
	40	PRO	PRO	PRO	PRO	PRO					PRO	PRO	---			PRO	PRO	PRO	PRO				PRO	PRO		
FR2	41		GLY	GLY	GLY	GLY					GLY	ASP	---			GLY	GLY	GLY	GLY				GLY	GLY		
	42		LYS	LYS	LYS	LYS					ILE	LYS	---			LYS	LYS	LYS	THR				LYS	LYS		
	43		ALA	ALA	ALA	ALA					ALA	ALA	---			ALA	ALA	ALA	ALA				VAL	ALA		
	44	PRO	PRO	PRO	PRO	PRO					PRO	PRO	---			PRO	PRO	PRO	PRO				PRO	PRO		
	45		LYS	LYS	LYS	LYS					LYS	LYS	---			LYS	LYS	LYS	LYS				LYS	LYS		
	46		LEU	LEU	LEU	LEU					LEU	LEU	---			LEU	LEU	LEU	LEU				LEU	LEU		
	47		LEU	MET	ILE	MET					MET	LEU	---			MET	ILE	ILE	ILE				MET	ILE		
	48	ILE	ILE	ILE	ILE	ILE					ILE	ILE	---			ILE	ILE	ILE	ILE				ILE	ILE		
	49		TYR	PHE	TYR	TYR					PHE	TYR	PHE	---		PHE	TYR	TYR	SER				TYR	TYR		
	50		ASP	ASP	ASP	GLU					ASP	ALA	ASP	---		ASP	GLY	GLY	GLU				ASP	GLU		
	51		VAL	VAL	VAL	GLY					VAL	VAL	VAL	---		VAL	VAL	PHE	VAL				VAL	VAL		
	52		ASN	SER	THR	ASN					SER	THR	ASN	---		THR	ASN	SER	ARG				ASP	SER		
	53		SER	GLU	TYR	LYS					ASN	PHE	SER	---		LYS	LYS	ASN	ASN				LYS	SER		
CDR2	54		ARG	ARG	ARG	ARG					ARG	ARG	ARG	---		ARG	ARG	ARG	ARG				ARG	ARG		
	55		PRO	PRO	PRO	PRO					PRO	PRO	PRO	---		PRO	PRO	PRO	PRO				PRO	PRO		
	56	SER	SER	SER	SER	SER					SER	SER	SER	---		SER	SER	SER	SER				SER	SER		
	57		GLY	GLY	GLY	GLY					GLY	GLY	GLY	---		GLY	GLY	GLY	GLY				GLY	GLY		
	58		ILE	VAL	ILE	VAL					VAL	ILE	VAL	---		VAL	VAL	VAL	VAL				VAL	VAL		
	59		SER	SER	SER	SER					SER	PRO	SER	---		PRO	PRO	PRO	SER				PRO	PRO		
	60		ASN	ASP	SER	ASN					ASN	LEU	HIS	---		ASP	TYR	LEU	ASP				ASP	ASP		
	61	ARG	ARG	ARG	ARG	ARG					ARG	ARG	ARG	---		ARG	ARG	ARG	ARG				ARG	ARG		
	62		PHE	PHE	PHE	PHE					PHE	PHE	PHE	---		LEU	PHE	PHE	PHE		PHE		PHE	PHE		
	63	SER	SER	SER	SER	SER					SER	SER	SER	---		SER	SER	SER	SER		SER		SER	SER		
	64	GLY	GLY	GLY	GLY	GLY					GLY	GLY	GLY	---		GLY	GLY	GLY	GLY		GLY		GLY	GLY		
	65	SER	SER	SER	SER	SER					SER	SER	SER	---		SER	SER	SER	SER		SER		SER	SER		
	66		LYS	LYS	ARG	LYS					LYS	LYS	LYS	---		SER	LYS	LYS	LYS		LYS		LYS	LYS		
	67		SER	SER	SER	SER					SER	SER	SER	---		SER	SER	SER	SER				SER	SER		
	68		GLY	GLY	GLY	GLY					GLY	GLY	GLY	---		GLY	GLY	GLY	ALA				ALA	GLY		
	69		ASN	ASN	ASN	LYS					ASN	ASN	ASN	---		ASP	ASN	ASP	ASN				ASN	ASX		
	70		THR	THR	THR	THR					THR	THR	THR	---		THR	THR	ALA	THR				THR	THR		
	71	ALA	ALA	ALA	ALA	ALA					ALA	ALA	ALA	---		ALA	ALA	ALA	ALA				ALA	ALA		
FR3	72		SER	SER	SER	SER					SER	SER	SER	---		SER	SER	SER	SER				SER	SER		
	73	LEU	LEU	LEU	LEU	LEU					LEU	LEU	LEU	---		LEU	LEU	LEU	LEU				LEU	LEU		
	74	THR	THR	THR	THR	THR					THR	THR	THR	---		THR	THR	THR	THR				THR	THR		
	75		ILE	ILE	ILE	ILE					ILE	ILE	ILE	---		ILE	ILE	ILE	ILE				ILE	ILE		
	76	SER	SER	SER	SER	SER					SER	SER	SER	---		SER	SER	SER	SER				SER	SER		
	77	GLY	GLY	GLY	GLY	GLY					GLY	GLY	GLY	---		GLY	GLY	GLY	GLY				GLY	GLY		
	78		LEU	LEU	LEU	LEU					LEU	LEU	LEU	---		LEU	LEU	LEU	LEU				LEU	LEU		
	79		GLN	GLN	GLN	GLN					GLN	LEU	GLN	---		ARG	GLN	GLN	GLN				GLN	GLN		
	80		ALA	ALA	ALA	VAL					ALA	PRO	ALA	---		ALA	ALA	VAL	ALA				ALA	ALA		
	81		GLU	GLU	GLU	GLU					GLU	ASP	GLU	---		ASP	GLU	GLU	GLU				ASN	GLU		
	82		ASP	ASP	ASP	ASP					ASP	ASP	ASP	---		ASP	ASP	ASP	ASP				ASN	ASP		
	83	GLU	GLU	GLU	GLU	GLU					GLU	GLU	GLU	---		GLU	GLU	GLU	GLU				GLU	GLU		
	84	ALA	ALA	ALA	ALA	ALA					ALA	ALA	ALA	---		ALA	ALA	ALA	ALA				ALA	ALA		
	85		ASP	ASP	ASP	ASP					ASP	ASP	HIS	---		ASP	HIS	ASP	ASP				ASP	ASX		
	86	TYR	TYR	TYR	TYR	TYR					TYR	TYR	TYR	---		TYR	TYR	TYR	TYR				TYR	TYR		
	87		TYR	TYR	TYR	TYR					TYR	PHE	PHE	---		TYR	TYR	TYR	TYR				TYR	TYR		
	88	CYS	CYS	CYS	CYS	CYS					CYS	CYS	CYS	---		CYS	CYS	CYS	CYS				CYS	CYS		
	89		SER	SER	SER	CYS					SER	MET	SER	---		CYS	CYS	SER	SER				SER	CYS		
	90		SER	SER	SER	SER					SER	SER	SER	---		SER	SER	SER	SER				SER	SER		
	91		PHE	TYR	TYR	TYR					PHE	TYR	TYR	---		TYR	TYR	TYR	TYR				TYR	TYR		
	92		THR	ALA	THR	ALA					THR	LEU	ARG	---		ALA	ALA	ALA	THR				GLY	ILE		
	93		THR	GLY	SER	GLY					ASP	SER	THR	---		GLY	GLY	ASP	SER				GLY	GLY		
	94		THR	SER	ASX	ASX					THR	ASP	SER	---		ARG	ARG	SER	SER				THR	SER		
	95		ASN	ASN	SER	SER					THR	ALA	GLY	---		TYR	PHE	SER	ASN				TYR	---		
CDR3	95A		SER	THR	THR	THR					GLN	SER	THR	---		SER	THR	---	SER				SER	---		
	95B		ARG	---	---	---					LEU	---	---	---		---	---	---	---				---	---		
	95C		---	---	---	---					---	---	---	---		---	---	---	---				---	---		
	95D		---	---	---	---					---	---	---	---		---	---	---	---				---	---		
	95E		---	---	---	---					---	---	---	---		---	---	---	---				---	---		
	95F		---	---	---	---					---	---	---	---		---	---	---	---				---	---		
	96		ALA	VAL	ARG	ARG					VAL	PHE	ILE	---		VAL	TRP	VAL	VAL				LEU	TYR		
	97		VAL	ILE	LEU	VAL	VAL	VAL			VAL	VAL	ILE	---		ILE	VAL	ILE	VAL				ILE	VAL		
	98	PHE	PHE	PHE	PHE	PHE	PHE	PHE			PHE	PHE	PHE	---		PHE	PHE	PHE	PHE				PHE	PHE		
	99	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY		GLY	GLY	GLY	---		GLY	GLY	GLY	GLY				GLY	GLY	GLY	
	100		GLY	GLY	GLY	GLY	THR	THR	THR		GLY	SER	GLY	---		GLY	GLY	ALA	GLY				GLY	THR	THR	
	101	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY		GLY	GLY	GLY	---		GLY	GLY	GLY	GLY				GLY	GLY	GLY	
FR4	102	THR	THR	THR	THR	THR	THR	THR	THR		THR	THR	THR	---		THR	THR	THR	THR				THR	THR	THR	
	103		LYS	LYS	LYS	ARG	GLN	ARG	LYS		LYS	LYS	TYR	---		LYS	ASN	LYS	LYS				LYS	LYS	LYS	
	104		LEU	LEU	LEU	VAL	VAL				LEU	VAL	VAL	---		LEU	LEU	LEU	LEU				LEU	VAL		
	105		SER	THR	THR	THR	THR				THR	THR	THR	---		THR	THR	THR	THR				THR	ILE		
	106	VAL	VAL	VAL	VAL	VAL					VAL	VAL	VAL	---		VAL	VAL	VAL	VAL				VAL	VAL		
	106A	LEU	LEU	LEU	LEU	LEU					LEU	LEU	LEU	---		LEU	LEU	LEU	LEU				LEU	LEU		
	107		GLY	GLY	ARG	SER					GLY	ARG	ARG	---		GLY	GLY	ARG	GLY				GLY	GLY		
	108		GLN	GLN		GLN					GLN	GLN		GLN			GLN		GLN				GLN	GLX		
	109	PRO	PRO	PRO		PRO					PRO	PRO		PRO			PRO		PRO				PRO	PRO		

HUMAN LAMBDA LIGHT CHAINS SUBGROUP II (cont'd)

		25 WAL	26 4A CL	# OF SEQUENCES	# OF AMINO ACIDS	OCCURRENCES OF MOST COMMON AMINO ACID	VARIABILITY
	0	---	---				
	1	PCA	gln	26	3	24(PCA)	3.3
	2	SER	thr	26	2	25(SER)	2.1
	3	val	val	26	3	23(ALA)	3.4
	4	LEU	val	26	2	25(LEU)	2.1
	5	THR	THR	26	3	23(THR)	3.4
	6	GLN	GLN	26	1 : 2	26(GLN) : 25(GLN)	1. : 2.1
	7	PRO	glu	26	3	24(PRO)	3.3
	8	pro	pro	26	3	18(ALA)	4.3
	9	SER	SER	26	2	25(SER)	2.1
FR1	10	---	---				
	11	ala	leu	26	3	23(VAL)	3.4
	12	SER	thr	26	2	25(SER)	2.1
	13	GLY	val	26	4	23(GLY)	4.5
	14	thr	SER	26	2	25(SER)	2.1
	15	PRO	PRO	26	2	25(PRO)	2.1
	16	GLY	GLY	26	1	26(GLY)	1.
	17	GLN	gly	26	4	23(GLN)	4.5
	18	arg	thr	26	3	23(SER)	3.4
	19		val	25	3	18(ILE)	4.2
	20		THR	25	1	25(THR)	1.
	21		leu	19	3	17(ILE)	3.4
	22		thr	18	2	17(SER)	2.1
	23		CYS	18	1	18(CYS)	1.
	24		ALA	15	4	9(THR)	6.7
	25		SER	15	2	14(GLY)	2.1
	26		SER	15	5	10(THR)	7.5
	27		THR	15	5	7(SER)	11.
	27A		---				
	27B		---				
	27C		---				
CDR1	27D		GLY	15	4	12(SER)	
	27E		ALA	15	4	11(ASP)	
	27F		VAL	15	2	14(VAL)	
	28		THR	15	5	10(GLY)	7.5
	29		SER	14	5	6(GLY)	12.
	30		GLY	14	6	9(TYR)	9.3
	31		TYR	14	7	8(ASN) : 7(ASN)	12. : 14.
	32		TYR	14	5	5(TYR)	14.
	33		PRO	13	3	11(VAL)	3.5
	34		ASN	13	2	12(SER)	2.2
	35		TRP	14	1	14(TRP)	1.
	36		PHE	14	2	10(TYR)	2.8
	37		GLN	14	1 : 2	14(GLN) : 13(GLN)	1. : 2.2
	38		GLN	14	2 : 3	13(GLN) : 12(GLN)	2.2 : 3.5
	39		LYS	14	5	10(HIS)	7.
	40		PRO	14	1	14(PRO)	1.
FR2	41		GLY	14	2	13(GLY)	2.2
	42		GLN	14	4	11(LYS)	5.1
	43		ALA	14	2	13(ALA)	2.2
	44		PRO	14	1	14(PRO)	1.
	45		ARG	14	2	13(LYS)	2.2
	46		ALA	14	3	12(LEU)	3.5
	47		LEU	14	3	5(+)	8.4
	48		ILE	14	1	14(ILE)	1.
	49		TYR	14	3	9(TYR)	4.7
	50		SER	14	5	7(ASP)	10.
	51		THR	14	4	11(VAL)	5.1
CDR2	52		SER	14	5	5(SER)	14.
	53		ASN	14	6	4(+)	21.
	54		LYS	14	2	13(ARG)	2.2
	55		HIS	14	2	13(PRO)	2.2
	56		SER	14	1	14(SER)	1.
	57		TRP	14	2	13(GLY)	2.2
	58		THR	14	3	10(VAL)	4.2
	59		PRO	14	2	7(+)	4.
	60		ALA	14	7	5(ASP)	20.
	61		ARG	14	1	14(ARG)	1.
	62		PHE	15	2	14(PHE)	2.1
	63		SER	15	1	15(SER)	1.
	64		GLY	15	1	15(GLY)	1.
	65		SER	15	1	15(SER)	1.
	66		LEU	15	3	13(LYS)	3.5
	67		LEU	14	2	13(SER)	2.2
	68		GLY	14	2	12(GLY)	2.3
	69		GLY	14	4	10(ASN) : 9(ASN)	5.6 : 6.2
	70		LYS	14	3	12(THR)	3.5
FR3	71		ALA	14	1	14(ALA)	1.
	72		ALA	14	2	13(SER)	2.2
	73		LEU	14	1	14(LEU)	1.
	74		THR	14	1	14(THR)	1.
	75		LEU	14	2	13(ILE)	2.2
	76		SER	14	1	14(SER)	1.
	77		GLY	14	1	14(GLY)	1.
	78		VAL	14	2	13(LEU)	2.2
	79		GLN	14	3	12(GLN)	3.5
	80		PRO	14	3	10(ALA)	4.2
	81		GLU	14	3	11(GLU)	3.8
	82		ASP	14	2	13(ASP)	2.2
	83		GLU	14	1	14(GLU)	1.
	84		ALA	14	1	14(ALA)	1.
	85		GLU	14	3 : 4	11(ASP) : 10(ASP)	3.8 : 5.6
	86		TYR	14	1	14(TYR)	1.
	87		TYR	14	2	12(TYR)	2.3
	88		CYS	14	1	14(CYS)	1.
	89		LEU	14	4	8(SER)	7.
	90		LEU	14	2	13(SER)	2.2
	91		TYR	14	2	12(TYR)	2.3
	92		TYR	14	7	5(ALA)	20.
	93		GLY	14	4	7(GLY)	8.
	94		GLY	14	5 : 6	5(SER)	14. : 17.
CDR3	95		ALA	13	7	3(+)	30.
	95A		---	11	3	5(+)	
	95B		---	2	2	1(+)	
	95C		---				
	95D		---				
	95E		---				
	95F		---				
	96		---	13	8	5(VAL)	21.
	97	VAL	---	16	3	10(VAL)	4.8
	98	PHE	---	16	1	16(PHE)	1.
	99	GLY	---	18	1	18(GLY)	1.
	100	SER	---	18	4	10(GLY)	7.2
	101	GLY	---	18	1	18(GLY)	1.
	102	THR	---	18	1	18(THR)	1.
FR4	103	LYS	---	18	5	13(LYS)	6.9
	104	VAL	---	15	2	9(LEU)	3.3
	105	THR	---	15	3	13(THR)	3.5
	106		---	13	1	13(VAL)	1.
	106A		---	13	1	13(LEU)	
	107		---	13	3	8(GLY)	4.9
	108		---	10	1 : 2	10(GLN) : 9(GLN)	1. : 2.2
	109		---	10	1	10(PRO)	1.

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NOTES: HUMAN LAMBDA LIGHT CHAINS SUBGROUP II

IDENTICAL SETS OF FRAMEWORK SEGMENTS:

FR1: SET 1: NIG-84[1],MES[2],WH[3],NEI[4],KAR[5],RIM[6],SLA[7]. (7 IDENTICAL)
SET 2: TRO[14],BOH[15]. (2 IDENTICAL)

FR2: SET 1: WH[3],BOH[15],NIG-58[16],BUR[22]. (4 IDENTICAL)

FR3:

FR4: SET 1: WH[3]. (IDENTICAL TO 1 HUMAN V-LAMBDA-I: NEWM[1]; AND 1 HUMAN V-LAMBDA-V: BO[1].)
SET 2: MES[2],ES492[8],TRO[14],VIL[17],WIN[21]. (5 IDENTICAL HUMAN V-LAMBDA-II; ALSO 4 HUMAN V-LAMBDA-I: BL2 'CL[6],RHE[10],OKA[12],NIG-51[19]; 4 HUMAN V-LAMBDA-III: HIL[1],CAP[4],BAU[12],DEL[14]; 1 HUMAN V-LAMBDA-IV: SH[1]; 3 HUMAN V-LAMBDA-VI: SUT[2],THO[4],LBV'CL[5]; AND 24 MOUSE V-LAMBDA: MOPC104E[1],J558[2],XS104[3],HOPC1[4],J698[5],H2061[6],W3159[7],Y5431[8],Y5485[9],Y5830[10],Y5669[11],MOPC511(L)[12],S178[13],Y5444[14],Y5606[15],S176[16],H2020[17],RPC20[18],IG 303LAMBDA'CL[19],S43'CL[21],S2H5'CL[38],S2E9'CL[39],S1F12'CL[40],IG 25LAMBDA'CL[41].)
SET 3: NIG-84[1]. (IDENTICAL TO 1 HUMAN V-LAMBDA-III: GAR[7].)

IDENTICAL SETS OF COMPLEMENTARITY DETERMINING REGIONS:

CDR1: SET 1: MES[2],VIL[17]. (2 IDENTICAL HUMAN V-LAMBDA-II; ALSO 1 HUMAN V-LAMBDA-V: MCG[3].)

CDR2: SET 1: NIG-84[1],TOG[10]. (2 IDENTICAL)

CDR3:

IDENTICAL SETS OF J-MINIGENES:

SET 1: MES[2],TRO[14]. (2 IDENTICAL HUMAN V-LAMBDA-II; ALSO 1 HUMAN V-LAMBDA-III: BAU[12].)
SET 2: ES492[8],VIL[17]. (2 IDENTICAL HUMAN V-LAMBDA-II; ALSO 1 HUMAN V-LAMBDA-III: DEL[14].)

SPECIFIC NOTES:

11) **SM:** IT HAS O-LINKED CARBOHYDRATE ATTACHED TO SER AT POSITION 22 AND N-LINKED CARBOHYDRATE ATTACHED TO ASX AT POSITION 25.

+ THE FOLLOWING WERE EQUALLY AND MOST FREQUENTLY OCCURRING:

AT POSITION	RESIDUES
47	(ILE,MET)
53	(LYS,ASN)
59	(PRO,SER)
95	(SER,ASN)
95A	(THR,SER)
95B	(LEU,ARG)

HUMAN LAMBDA LIGHT CHAINS SUBGROUP III

		INVARIANT RESIDUES	1 HIL	2 YO	3 PS	4 CAP	5 LOY A	6 LOY G	7 GAR	8 CH	9 X (PET)	10 KERN	11 TA	12 BAU	13 AMYLOID 758	14 DEL	15 LYN	16 NIG -68	17 AMYLOID 808	18 MOT #	19 WIG	20 WHI	21 DU	22 LON
	0		---	---	---	---	---	---	---	---	---	---	---	---	---	---	---	---	---	#	---	---	---	---
	1		SER	SER	SER	SER	SER	SER	SER	SER	---	---	SER	---	---	---	---	---	---	phe	SER	---	---	---
	2	TYR(.96)	TYR	TYR	TYR	TYR	TYR	TYR	TYR	TYR	TYR	TYR	TYR	TYR	TYR	TYR	TYR	TYR	TYR	TYR	phe	TYR	TYR	TYR
	3		GLU	GLU	GLU	GLU	GLU	GLU	GLU	GLU	asp	ala	ala	gly	asp	val	GLU	asp	asp	GLU	gly	val	GLX	ser
	4	LEU(.96)	LEU	LEU	LEU	LEU	LEU	LEU	LEU	LEU	LEU	LEU	LEU	LEU	LEU	LEU	LEU	LEU	LEU	LEU	val	LEU	LEU	LEU
	5		THR	THR	THR	THR	THR	THR	lys	THR	THR	THR	THR	THR	THR	ser	THR	THR	THR	THR	ser	THR	THR	THR
	6		GLN	GLN	GLN	GLN	GLN	GLN	GLN	GLN	GLN	GLN	GLN	GLN	GLN	GLN	GLN	GLN	GLN	GLN	GLN	GLX	GLX	GLN
	7		PRO	PRO	PRO	PRO	PRO	PRO	PRO	PRO	PRO	PRO	PRO	PRO	PRO	PRO	PRO	ala		PRO	PRO	ala	PRO	PRO
	8	PRO	PRO	PRO	PRO	PRO	PRO	PRO	PRO	PRO	PRO	PRO	PRO	PRO	PRO	PRO	PRO	PRO	PRO	PRO	PRO	PRO	PRO	PRO
	9	SER	SER	SER	SER	SER	SER	SER	SER	SER	SER	SER	SER	SER	SER	SER	SER	SER	SER	SER	SER	SER	SER	SER
	10		---	---	---	---	---	---	---	---	---	---	---	---	---	---	---	---	---	---	---	---	---	---
FR1	11		VAL	VAL	VAL	VAL	VAL	VAL	VAL	VAL	VAL	VAL	VAL	leu	met	VAL	VAL	leu	VAL	VAL	VAL	leu	VAL	VAL
	12	SER	SER	SER	SER	SER	SER	SER	SER	SER	SER	SER	SER	SER	SER	SER	SER	SER	SER	SER	SER	SER	SER	SER
	13	VAL(.96)	VAL	VAL	VAL	VAL	VAL	VAL	VAL	VAL	VAL	VAL	VAL	VAL	VAL	VAL	VAL	VAL	leu	VAL	VAL	VAL	VAL	VAL
	14		SER	SER	SER	SER	SER	SER	SER	SER	SER	SER	SER	SER	SER	ala	phe	SER	SER	ala	SER	ala	SER	SER
	15	PRO(.95)	PRO	PRO	PRO	PRO	PRO	PRO	PRO	PRO	PRO	PRO	PRO	PRO	PRO	PRO	PRO	PRO	PRO	ala	PRO	PRO	PRO	PRO
	16	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	
	17		GLN	GLN	GLN	GLN	GLN	GLN	GLN	GLN	GLN	GLN	GLN	GLN	GLX	GLN	GLN	GLN		GLN	GLN	GLX	GLX	
	18		THR	THR	THR	THR	THR	THR	THR	THR	THR	THR	THR	THR	THR	THR	pro	THR	THR	THR	THR	THR		
	19	ALA(.95)	ALA	ALA	ALA	ALA	ALA	ALA	ALA	ALA	ALA	ALA	ALA	ALA	ALA	ALA	gly	ALA	ALA	ALA	ALA	ALA		
	20		ARG	ARG	ARG	ARG	ser	ser	ARG	ARG	ser	val		ser	ser	ARG	thr	tyr		met	ser	ARG		
	21	ILE	ILE	ILE	ILE	ILE	ILE	ILE	ILE		ILE	ILE		ILE	THR	ILE	ILE	ILE	ILE	ILE	ILE	ILE		
	22	THR	THR	THR	THR	THR	THR	THR	THR		THR	THR		THR		THR	THR	THR	THR	THR	THR	THR		
	23	CYS	CYS	CYS	CYS	CYS	CYS	CYS	CYS		CYS	CYS		CYS		CYS	CYS	CYS		CYS	CYS	CYS		
	24		SER	SER	SER	SER	SER	SER	SER		SER	SER		SER	SER	GLY	SER	SER		GLU		GLX		
	25		ALA	GLY	GLY	GLY	GLY	GLY	GLY		GLY	GLY		GLY	GLY	GLY	GLY	GLY		GLY				
	26		ASN	ASP	ASP	ASP	ASP	ASX	ASP		ASP	ASP		ASP	GLX	ASP	ASP	ASP		ASN		ASX		
	27		ALA	ALA	ALA	ALA	---	---	VAL		LYS	ASN		LYS	ASX	GLY	ALA	ASN		ASP		ASX		
	27A		---	---	---	---	---	---	---		---	---		---	---	---	---	---		---		---		
	27B		---	---	---	---	---	---	---		---	---		---	---	---	---	---		---		---		
CDR1	27C		---	---	---	---	---	---	---		---	---		---	---	---	---	---		---		---		
	27D		---	---	---	---	---	---	---		---	---		---	---	---	---	---		---		---		
	27E		---	---	---	---	---	---	---		---	---		---	---	---	---	---		---		---		
	27F		---	---	---	---	---	---	---		---	---		---	---	---	---	---		---		---		
	28		LEU	LEU	LEU	LEU	LEU	LEU	LEU		LEU	LEU		LEU	LEU	ILE	LEU	LEU		ILE		ILE		
	29		PRO	PRO	THR	PRO	---	---	PRO		GLY	GLU		GLY		GLY	SER	GLY		GLY		GLX		
	30		ASN	ASP	ASN	ALA	GLX	GLX	LYS		ASP	LYS		GLU		GLY	ASP	ASN		GLU		GLX		
	31		GLN	LEU	LYS	GLU	GLX	GLX	LYS		LYS	THR		GLN		LYS	LYS	GLU		ARG				
	32		TYR	TYR	TYR	TYR			TYR		ASP	PHE		TYR		SER	TYR	PHE		SER			TYR	
	33		ALA	VAL	ALA	ALA			ALA		VAL	VAL		VAL		VAL	VAL	VAL		VAL			VAL	
	34		TYR		TYR	TYR			TYR		CYS	SER		CYS		HIS		SER		HIS			CYS	
	35	TRP	TRP	TRP	TRP	TRP			TRP		TRP	TRP		TRP		TRP	TRP	TRP		TRP			TRP	
	36		TYR	TYR		TYR			TYR		TYR	PHE		TYR		TYR	TYR	TYR		TYR				
	37		GLN	GLN		GLN			GLN		GLN	GLN		GLN		GLN	GLX	GLN		GLN				
	38		GLN	GLN		GLN			GLU		GLN	GLN		GLN		GLN	HIS	GLN		GLN				
	39		LYS	LYS		LYS			ARG		ARG	ARG		LYS		LYS	LYS	ARG		LYS				
	40		PRO			PRO			SER		PRO	PRO		PRO		PRO	PRO	PRO		PRO				
FR2	41	GLY	GLY			GLY			GLY		GLY	GLY		GLY		GLY	GLY	GLY		GLY				
	42		ARG			GLN			GLN		GLN	GLN		GLN		GLN		GLX		GLN				
	43		ALA			ALA			ALA		SER	SER		SER		ALA		SER		ALA				
	44	PRO	PRO			PRO			PRO		PRO	PRO		PRO		PRO	PRO	PRO		PRO				
	45		VAL			VAL			VAL		VAL	LEU		VAL		VAL	LEU	ALA		VAL				
	46		MET			MET			LEU		LEU	LEU		LEU		LEU		LEU		PRO				
	47	VAL	VAL			VAL			VAL		VAL	VAL		VAL		VAL	VAL	VAL		VAL				
	48		ILE			ILE			VAL		ILE	ILE		ILE		VAL	ILE	ILE		ILE				
	49		TYR			TYR			TYR		TYR	TYR		TYR		HIS	TYR	TYR		TYR				
	50		LYS			GLU			GLU		GLN	HIS		HIS		GLU	GLX	ASX		ASP				
CDR2	51		ASP			THR			ASP	ASP	ASP	THR		ASP		ASP		THR		ASP				
	52		THR			ASN			SER	THR	ASN	SER		SER		ASN	THR	SER		ASP				
	53		GLN			LYS			GLY	GLY	GLN	GLU		LYS		ASP	LYS	LYS		ASP				
	54	ARG	ARG			ARG			ARG	ARG	ARG	ARG		ARG		ARG	ARG	ARG		ARG				
	55		PRO			PRO			PRO	PRO	SER	PRO		PRO		PRO	PRO	PRO		PRO				
	56		SER			SER			SER	SER	SER	SER		SER		ALA		SER		SER				
	57		GLY			GLY			GLU	THR	GLY	GLU		GLY		GLY	GLY	GLY		GLY				
	58		ILE			ILE			ILE	ILE	ILE	ILE		ILE		ILE		ILE		VAL				
	59	PRO	PRO			PRO			PRO	PRO	PRO	PRO		PRO		PRO		PRO		PRO				
	60		GLN			GLU			GLU	GLU	GLU	GLU		GLU		GLU	GLX	GLU		ALA				
	61	ARG	ARG			ARG			ARG	ARG	ARG	ARG		ARG		ARG	ARG	ARG		ARG				
	62	PHE	PHE			PHE			PHE	PHE	PHE	PHE		PHE		PHE	PHE	PHE		PHE				
	63	SER	SER			SER			SER	SER	SER	SER		SER		SER		SER		SER				
	64		SER			GLY			GLY	GLY	GLY	GLY		GLY		GLY		GLY		GLY				
	65		SER			SER			SER	SER	SER	SER		SER		SER		SER		TYR				
	66		THR			THR			SER	THR	ASN	SER		ASN		ASN		LYS		ASN				
	67	SER	SER			SER			SER	SER	SER	SER		SER		SER		SER		SER				
	68	GLY	GLY			GLY			GLY	GLY	GLY	GLY		GLY		GLY		GLY		GLY				
	69		THR			THR			THR	THR	ASN	ALA		THR		ASN		ASN		ASN				
	70		THR			THR			LYS	THR	THR	THR		THR		THR		THR		SER				
	71		VAL			VAL			ALA	ALA	ALA	ALA		ALA		ALA		ALA		ALA				
FR3	72		THR			THR			THR	THR	THR	THR		THR		ALA		THR		ILE				
	73	LEU	LEU			LEU			LEU	LEU	LEU	LEU		LEU		LEU		LEU		LEU				
	74	THR	THR			THR			THR	THR	THR	THR		THR		THR		THR		THR				
	75	ILE	ILE			ILE			ILE	ILE	ILE	ILE		ILE		ILE		ILE		ILE				
	76		SER			SER			SER	SER	SER	SER		SER		SER		SER		ASN				
	77		GLY			GLY			GLY	GLY	GLY	GLY		GLY		ARG		GLY		ARG				
	78		VAL			VAL			ALA	VAL	THR	ALA		THR		VAL		THR		VAL				
	79		GLN			GLN			GLN	GLN	GLN	GLN		GLN		GLU		GLU		GLU				
	80		ALA			ALA			VAL	ALA	ALA	SER		ALA		ALA		SER		ALA				
	81		GLU			GLU			GLU	ASN	MET	VAL		MET		GLY		MET		GLY				
	82		ASP			ASP			ASP	ASX	ASP	ASP		ASP		ASP		ASX		ASP				
	83		GLU			GLU			GLU	GLX	GLU	GLU		GLU		GLU		GLU		GLU				
	84	ALA	ALA			ALA			ALA	ALA	ALA	ALA		ALA		ALA		ALA		ALA				
	85		ASP			ASP			ASP	ASX	ASP	ASP		ASP		ASP		ASX		ASP				
	86	TYR	TYR			TYR			TYR	TYR	TYR	TYR		TYR		TYR		TYR		TYR				
	87		TYR			TYR			TYR	TYR	TYR	PHE		TYR		TYR		TYR		PHE				
	88	CYS	CYS			CYS			CYS	CYS	CYS	CYS		CYS		CYS		CYS		CYS				
	89		GLN			SER			SER	GLX	GLN	GLN		GLN		GLU		GLX		GLN				
	90		ALA			SER			THR	SER	ALA	THR		ALA		VAL		ALA		SER				
	91		TRP			ALA			ASP	ALA	TRP	TRP		TRP		TRP		TRP		TRP				
	92		ASP			ASP			ILE	ASN	ASP	ASP		ASP		ASP		ASX		ASP				
	93		ASN			SER			ASN	SER	SER	THR		SER		ASP		GLX		ASN				
	94		SER			SER			GLY	ARG	MET	ILE		TYR		ARG		ILE		GLY				
	95		ALA			GLN			TYR		SER	THR		THR		THR		ARG		SER				
	95A		---			GLY			---		---	---		---		ALA		ASP		TYR				
CDR3	95B		---			---			---		---	---		---		HIS		---		GLU				
	95C		---			---			---		---	---		---		---		---		---				
	95D		---			---			---		---	---		---		---		---		---				
	95E		---			---			---		---	---		---		---		---		---				
	95F		---			---			---		---	---		---		---		---		---				
	96		SER			MET			PRO		VAL	ALA		VAL		VAL		VAL		VAL				
	97		ILE			VAL			LEU		VAL	ILE		ILE		VAL		VAL		VAL	VAL			
	98	PHE	PHE			PHE			PHE		PHE	PHE		PHE		PHE		PHE		PHE	PHE			
	99	GLY	GLY			GLY			GLY	GLY	GLY	GLY		GLY		GLY		GLY		GLY	GLY			
	100		GLY			GLY			GLY	GLY	GLY	GLY		GLY		GLY		GLY		THR	ALA			
	101	GLY	GLY			GLY			GLY	GLY	GLY	GLY		GLY		GLY		GLY		GLY	GLY			
FR4	102	THR	THR			THR			THR	THR	THR	THR		THR		THR		THR		THR	THR			
	103		LYS			LYS			LYS	LYS	ARG	LYS		LYS		LYS		LYS		MET	THR			
	104		LEU			LEU			LEU	LEU	LEU	LEU		LEU		LEU		LEU		VAL				
	105		THR			THR			SER	THR	THR	THR		THR		THR		THR		THR				
	106	VAL	VAL			VAL			VAL	VAL	VAL	VAL		VAL		VAL		VAL		VAL				
	106A	LEU	LEU			LEU			LEU	LEU	LEU	LEU		LEU		LEU		LEU		LEU				
	107		GLY			GLY			GLY		SER	SER		GLY		GLY				GLY				
	108	GLN	GLN			GLN			GLN		GLN	GLN		GLN						GLN				
	109	PRO	PRO			PRO			PRO		PRO	PRO		PRO						PRO				

HUMAN LAMBDA LIGHT CHAINS SUBGROUP III (cont'd)

		23 SG	24 GIM	25 111	26 119	27 VIN	28 MIL	# OF SEQUENCES	# OF AMINO ACIDS	OCCURRENCES OF MOST COMMON AMINO ACID	VARIABILITY
	0	---	---	---	---	---					
	1	tyr	---	---	---	---		12	3	10(SER)	3.6
	2	TYR	TYR	TYR	TYR	TYR		27	2	26(TYR)	2.1
	3	val	val	GLU	GLX			26	6 : 7	13(GLU) : 11(GLU)	12. : 17.
	4	LEU	LEU	LEU	LEU			26	2	25(LEU)	2.1
	5	THR	THR	THR	THR			26	3	23(THR)	3.4
	6	GLN	GLX	GLN	GLX			26	1 : 2	26(GLN) : 22(GLN)	1. : 2.4
	7	PRO	PRO	PRO	PRO			25	2	23(PRO)	2.2
	8	PRO	PRO	PRO	PRO			26	1	26(PRO)	1.
	9	SER	SER					24	1	24(SER)	1.
	10	---	---								
FR1	11	VAL	VAL					24	3	20(VAL)	3.6
	12	SER	SER					24	1	24(SER)	1.
	13	VAL	VAL					24	2	23(VAL)	2.1
	14							22	3	18(SER)	3.7
	15							22	2	21(PRO)	2.1
	16							21	1	21(GLY)	1.
	17							20	1 : 2	20(GLN) : 17(GLN)	1. : 2.4
	18					met		21	3	19(THR)	3.3
	19							20	2	19(ALA)	2.1
	20							18	6	8(ARG)	14.
	21						ILE	19	1	19(ILE)	1.
	22						THR	19	1	19(THR)	1.
	23						CYS	17	1	17(CYS)	1.
	24						GLY	17	3 : 4	13(SER)	3.9 : 5.2
	25						GLY	16	2	15(GLY)	2.1
	26						ASP	17	3	14(ASP) : 12(ASP)	3.6 : 4.3
	27						GLU	15	7	5(ALA)	21.
	27A										
	27B										
CDR1	27C										
	27D										
	27E										
	27F										
	28							16	2	13(LEU)	2.5
	29							13	5 : 6	5(GLY)	13. : 16.
	30							15	6 : 7	5(GLU) : 3(+)	18. : 35.
	31							14	6	5(LYS)	17.
	32							13	4	8(TYR)	6.5
	33							13	2	9(VAL)	2.9
	34							11	4	4(TYR)	11.
	35							13	1	13(TRP)	1.
	36							11	2	10(TYR)	2.2
	37							11	1 : 2	11(GLN) : 10(GLN)	1. : 2.2
	38							11	3	9(GLN)	3.7
	39							11	2	7(LYS)	3.1
	40							10	2	9(PRO)	2.2
	41							10	1	10(GLY)	1.
FR2	42							9	2 : 3	8(GLN) : 7(GLN)	2.3 : 3.9
	43							9	2	5(ALA)	3.6
	44							10	1	10(PRO)	1.
	45							10	3	7(VAL)	4.3
	46							9	3	6(LEU)	4.5
	47							10	1	10(VAL)	1.
	48							10	2	8(ILE)	2.5
	49							10	2	9(TYR)	2.2
	50							10	5 : 6	4(GLU) : 3(GLU)	13. : 20.
	51							10	2	7(ASP)	2.9
	52							11	4	4(SER)	11.
CDR2	53							11	5	4(LYS)	14.
	54							11	1	11(ARG)	1.
	55							11	2	10(PRO)	2.2
	56							10	2	9(SER)	2.2
	57							11	3	8(GLY)	4.1
	58							10	2	9(ILE)	2.2
	59							10	1	10(PRO)	1.
	60							11	3	9(GLU) : 8(GLU)	3.7 : 4.1
	61							11	1	11(ARG)	1.
	62							11	1	11(PHE)	1.
	63							10	1	10(SER)	1.
	64							10	2	9(GLY)	2.2
	65							10	2	9(SER)	2.2
	66							10	4	4(ASN)	10.
	67							10	1	10(SER)	1.
	68							10	1	10(GLY)	1.
	69							10	3	5(THR)	6.
	70							10	3	8(THR)	3.8
	71							10	2	8(ALA)	2.5
FR3	72							10	3	8(THR)	3.8
	73							10	1	10(LEU)	1.
	74							10	1	10(THR)	1.
	75							10	1	10(ILE)	1.
	76							10	2	9(SER)	2.2
	77							10	2	8(GLY)	2.5
	78							10	3	5(VAL)	6.
	79							10	2	7(GLN)	2.9
	80							10	3	7(ALA)	4.3
	81							10	5	3(+)	17.
	82							10	1 : 2	10(ASP) : 8(ASP)	1. : 2.5
	83							10	1 : 2	10(GLU) : 9(GLU)	1. : 2.2
	84							10	1	10(ALA)	1.
	85							10	1 : 2	10(ASP) : 8(ASP)	1. : 2.5
	86							10	1	10(TYR)	1.
	87							10	2	8(TYR)	2.5
	88							10	1	10(CYS)	1.
	89							10	3	7(GLN) : 5(GLN)	4.3 : 6.
	90							10	4	4(ALA)	10.
	91							10	3	7(TRP)	4.3
	92							10	3	8(ASP) : 7(ASP)	3.8 : 4.3
	93							10	5	4(SER)	13.
	94							10	6	2(+)	30.
	95							9	6	3(THR)	18.
	95A							4	4	1(+)	
CDR3	95B							2	2	1(+)	
	95C										
	95D										
	95E										
	95F										
	96							9	5	5(VAL)	9.
	97							10	3	6(VAL)	5.
	98							10	1	10(PHE)	1.
	99							11	1	11(GLY)	1.
	100							11	3	9(GLY)	3.7
	101							11	1	11(GLY)	1.
	102							11	1	11(THR)	1.
FR4	103							11	4	8(LYS)	5.5
	104							10	2	9(LEU)	2.2
	105							10	2	9(THR)	2.2
	106							10	1	10(VAL)	1.
	106A							10	1	10(LEU)	
	107							8	2	6(GLY)	2.7
	108							7	1	7(GLN)	1.
	109							7	1	7(PRO)	1.

ANTIBODY SPECIFICITIES: HUMAN LAMBDA LIGHT CHAINS SUBGROUP III

7) **GAR:** ANTI-RIBOFLAVIN

REFERENCE: HUMAN LAMBDA LIGHT CHAINS SUBGROUP III

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2) **YO:** TISCHENDORF,F.W.,TISCHENDORF,M.M. & WITTMANN-LIEBOLD,B. (1976) Z.NATURFORSCH,31C,758-760.
3) **PS:** KOCHWA,S.,TERRY,W.D.,CAPRA,J.D. & YANG,N.Y. (1971) ANN.N.Y.ACAD.SCI.,190,49-70. (CHECKED BY AUTHOR)
4) **CAP:** ZHU,D.,KIM,H.S. & DEUTSCH,H.F. (1983) MOL.IMMUNOL.,20,1107-1116.
5) **LOY A:** WOLFENSTEIN-TODEL,C.,FRANKLIN,E.C. & RUDDERS,R.A. (1974) J.IMMUNOL.,112,871-876. (CHECKED BY AUTHOR)
6) **LOY G:** WOLFENSTEIN-TODEL,C.,FRANKLIN,E.C. & RUDDERS,R.A. (1974) J.IMMUNOL.,112,871-876. (CHECKED BY AUTHOR)
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9) **X(PET):** MILSTEIN,C.,CLEGG,J.B. & JARVIS,J.M. (1968) BIOCHEM.J.,110,631-652. (CHECKED BY AUTHOR)
10) **KERN:** PONSTINGL,H.,HESS,M. & HILSCHMANN,N. (1968) Z.PHYSIOL.CHEM.,349,867-871; (1971) Z.PHYSIOL.CHEM.,352,247-266. (CHECKED BY AUTHOR)
11) **TA:** TONNELLE,C. (1973) BIOCHIM.BIOPHYS.RES.COMM.,55,1112-1116. (CHECKED BY AUTHOR 11/16/80)
12) **BAU:** BACZKO,K.,BRAUN,D.G.,HESS,M. & HILSCHMANN,N. (1970) Z.PHYSIOL.CHEM.,351,763-767; BACZKO,K.,BRAUN,D.G. & HILSCHMANN,N. (1974) Z.PHYSIOL.CHEM.,355,131-154. (CHECKED BY AUTHOR)
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14) **DEL:** EULITZ,M. (1974) EUR.J.BIOCHEM.,50,49-69. (CHECKED BY AUTHOR 10/18/77)
15) **LYN:** MEINKE,G.C.,SIGRIST,P.H. & SPIEGELBERG,H.L. (1974) IMMUNOCHEM.,11,457-460. (CHECKED BY AUTHOR WHO PROVIDED ADDITIONAL RESIDUES TO THOSE PUBLISHED); MEINKE,G.C. & SPIEGELBERG,H.L. (1976) IMMUNOCHEM.,13,915-919. (CHECKED BY AUTHOR 10/17/77)
16) **NIG-68:** KAMETANI,F.,YOSHIMURA,K.,TONOIKE,H.,HOSHI,A.,SHINODA,T. & ISOBE,T. (1985) BIOCHEM.BIOPHYS.RES.COMMUN.,126,848-852.
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18) **MOT:** KOJIMA,M.,ODANI,S. & IKENAKA,T. (1980) MOL.IMMUNOL.,17,1407-1414.
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23) **SG:** TISCHENDORF,F.W.,TISCHENDORF,M.M. & WITTMANN-LIEBOLD,B. (1976) Z.NATURFORSCH,31C,758-760.
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25) **111:** LANGER,B.,STEINMETZ-KAYNE,M. & HILSCHMANN,N. (1968) Z.PHYSIOL.CHEM.,349,945-951. (CHECKED BY AUTHOR)
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27) **VIN:** PINK,J.R.L. & MILSTEIN,C. (1969) PROC. 5TH FEBS SYMP.,15,177-182. (CHECKED BY AUTHOR)
28) **MIL:** LANGER,B.,STEINMETZ-KAYNE,M. & HILSCHMANN,N. (1968) Z.PHYSIOL.CHEM.,349,945-951. (CHECKED BY AUTHOR)

NOTES: HUMAN LAMBDA LIGHT CHAINS SUBGROUP III

IDENTICAL SETS OF FRAMEWORK SEGMENTS:

FR1: SET 1: HIL[1],YO[2],PS[3],CAP[4]. (4 IDENTICAL)
SET 2: LOY A[5],LOY G[6]. (2 IDENTICAL)

FR2:

FR3:

FR4: SET 1: HIL[1],CAP[4],BAU[12],DEL[14]. (4 IDENTICAL HUMAN V-LAMBDA-III; ALSO 4 HUMAN V-LAMBDA-I: BL2 'CL[6],RHE[10],OKA[12], NIG-51[19]; 5 HUMAN V-LAMBDA-II: MES[2],ES492[8],TRO[14],VIL[17],WIN[21]; 1 HUMAN V-LAMBDA-IV: SH[1]; 3 HUMAN V-LAMBDA-VI: SUT[2],THO[4],LBV'CL[5]; AND 24 MOUSE V-LAMBDA: MOPC104E[1],J558[2],XS104[3],HOPC1[4],J698[5],H2061[6], W3159[7],Y5431[8],Y5485[9],Y5830[10],Y5669[11],MOPC511(L)[12],S178[13],Y5444[14],Y5606[15],S176[16],H2020[17], RPC20[18],IG 303LAMBDA'CL[19],S43'CL[21],S2H5'CL[38],S2E9'CL[39],S1F12'CL[40],IG 25LAMBDA'CL[41].)
SET 2: GAR[7]. (IDENTICAL TO 1 HUMAN V-LAMBDA-II: NIG-84[1].)
SET 3: KERN[10]. (IDENTICAL TO 1 HUMAN V-LAMBDA-VI: NIG-48[10].)

IDENTICAL SETS OF J-MINIGENES:

SET 1: BAU[12]. (IDENTICAL TO 2 HUMAN V-LAMBDA-II: MES[2],TRO[14].)
SET 2: DEL[14]. (IDENTICAL TO 2 HUMAN V-LAMBDA-II: ES492[8],VIL[17].)

SPECIFIC NOTES:

18) **MOT:** THERE ARE TWO RESIDUES IN FRONT OF POSITION 1; THEY ARE VAL AND THR.

+ THE FOLLOWING WERE EQUALLY AND MOST FREQUENTLY OCCURRING:

AT POSITION	RESIDUES
30	(ASP,ASN,GLN)
81	(MET,GLU)
94	(ILE,ARG,SER,GLY)
95A	(TYR,ALA,GLY,ASP)
95B	(HIS,GLU)

HUMAN LAMBDA LIGHT CHAINS SUBGROUP IV

		INVARIANT RESIDUES	1 SH	2 NEV	3 USH	4 PFA	5 FRA'	# OF SEQUENCES	# OF AMINO ACIDS	OCCURRENCES OF MOST COMMON AMINO ACID	VARIABILITY
	0		---	---	---	---	---				
	1		---	---	---	---	---				
	2	SER	SER	SER	SER	SER	---	4	1	4(SER)	1.
	3		GLU	GLU	GLU	GLU	ala	5	2	4(GLU)	2.5
	4	LEU	LEU	LEU	LEU	LEU	LEU	5	1	5(LEU)	1.
	5		THR	THR	THR	THR	val	5	2	4(THR)	2.5
	6	GLN	GLN	GLN	GLN	GLN	GLN	5	1	5(GLN)	1.
	7		ASP	ASX	pro	pro	pro	5	2 : 3	3(PRO)	3.3 : 5.
	8		PRO	PRO	PRO	PRO	ala	5	2	4(PRO)	2.5
	9		ALA	ALA	ser	ser	ser	5	2	3(SER)	3.3
	10		---	---	---	---	---				
F	11	VAL	VAL	VAL	VAL	VAL	VAL	5	1	5(VAL)	1.
R	12		SER	SER	SER	SER	glx	5	2	4(SER)	2.5
1	13		VAL	VAL	VAL	VAL	gly	5	2	4(VAL)	2.5
	14		ALA	ALA	ser	ser	ALA	5	2	3(ALA)	3.3
	15		LEU	LEU	pro	pro	pro	5	2	3(PRO)	3.3
	16	GLY	GLY	GLY	GLY	GLY	GLY	5	1	5(GLY)	1.
	17		GLN	GLX	GLN	GLN	GLX	5	1 : 2	5(GLN) : 3(GLN)	1. : 3.3
	18		THR	THR	THR	THR	ser	5	2	4(THR)	2.5
	19		VAL	VAL	ala	ala	ile	5	3	2(+)	7.5
	20		ARG	ARG	ser	val	ala	5	4	2(ARG)	10.
	21	ILE	ILE	ILE	ILE	ILE	ILE	5	1	5(ILE)	1.
	22		THR	THR	THR	THR	gly	5	2	4(THR)	2.5
	23	CYS	CYS		CYS	CYS	CYS	4	1	4(CYS)	1.
	24		GLN		SER	SER	ILE	4	3	2(SER)	6.
	25	GLY	GLY		GLY	GLY	GLY	4	1	4(GLY)	1.
	26		ASP		ASP	ASP	ILE	4	2	3(ASP)	2.7
	27		SER		LYS	LYS	SER	4	2	2(+)	4.
	27A		---		---	---	---				
	27B		---		---	---	---				
C	27C		---		---	---	---				
D	27D		---		---	---	---				
R	27E		---		---	---					
1	27F		---		---	---	ASX	1	1	1(ASN) : 1(ASP)	
	28		LEU		LEU	LEU	ILE	4	2	3(LEU)	2.7
	29		ARG		GLY	GLY	GLY	4	2	3(GLY)	2.7
	30		GLY		ASP	GLN	ALA	4	4	1(+)	16.
	31		TYR		ASN	ALA	TYR	4	3	2(TYR)	6.
	32		ASP		TYR		ASX	3	2 : 3	2(ASP) : 1(+)	3. : 9.
	33		ALA		ALA		TYR	3	2	2(ALA)	3.
	34		ALA		SER		ILE	3	3	1(+)	9.
	35	TRP	TRP		TRP	TRP		3	1	3(TRP)	1.
	36	TYR	TYR		TYR	TYR		3	1	3(TYR)	1.
	37	GLN	GLN		GLN			2	1	2(GLN)	1.
	38	GLN	GLN		GLN			2	1	2(GLN)	1.
	39	LYS	LYS		LYS			2	1	2(LYS)	1.
	40		PRO					1	1	1(PRO)	
F	41		GLY					1	1	1(GLY)	
R	42		GLN					1	1	1(GLN)	
2	43		ALA					1	1	1(ALA)	
	44		PRO					1	1	1(PRO)	
	45		LEU					1	1	1(LEU)	
	46		LEU					1	1	1(LEU)	
	47		VAL					1	1	1(VAL)	
	48		ILE					1	1	1(ILE)	
	49		TYR					1	1	1(TYR)	
	50		GLY					1	1	1(GLY)	
	51		ARG					1	1	1(ARG)	
C	52		ASN					1	1	1(ASN)	
D	53		ASN					1	1	1(ASN)	
R	54		ARG					1	1	1(ARG)	
2	55		PRO					1	1	1(PRO)	
	56		SER					1	1	1(SER)	
	57		GLY					1	1	1(GLY)	
	58		ILE					1	1	1(ILE)	
	59		PRO					1	1	1(PRO)	
	60		ASP					1	1	1(ASP)	
	61		ARG					1	1	1(ARG)	
	62		PHE					1	1	1(PHE)	
	63		SER					1	1	1(SER)	
	64		GLY					1	1	1(GLY)	
	65		SER					1	1	1(SER)	
	66		SER					1	1	1(SER)	
	67		SER					1	1	1(SER)	
	68		GLY					1	1	1(GLY)	
	69		HIS					1	1	1(HIS)	
	70		THR					1	1	1(THR)	
	71		ALA					1	1	1(ALA)	
F	72		SER					1	1	1(SER)	
R	73		LEU					1	1	1(LEU)	
3	74		THR					1	1	1(THR)	
	75		ILE					1	1	1(ILE)	
	76		THR					1	1	1(THR)	
	77		GLY					1	1	1(GLY)	
	78		ALA					1	1	1(ALA)	
	79		GLN					1	1	1(GLN)	
	80		ALA					1	1	1(ALA)	
	81		GLU					1	1	1(GLU)	
	82		ASP					1	1	1(ASP)	
	83		GLU					1	1	1(GLU)	
	84		ALA					1	1	1(ALA)	
	85		ASP					1	1	1(ASP)	
	86		TYR					1	1	1(TYR)	
	87		TYR					1	1	1(TYR)	
	88		CYS					1	1	1(CYS)	
	89		ASN					1	1	1(ASN)	
	90		SER					1	1	1(SER)	
	91		ARG					1	1	1(ARG)	
	92		ASP					1	1	1(ASP)	
	93		SER					1	1	1(SER)	
	94		SER					1	1	1(SER)	
C	95		GLY					1	1	1(GLY)	
D	95A		LYS					1	1	1(LYS)	
R	95B		HIS					1	1	1(HIS)	
3	95C		---								
	95D		---								
	95E		---								
	95F		---								
	96		VAL					1	1	1(VAL)	
	97		LEU					1	1	1(LEU)	
	98		PHE					1	1	1(PHE)	
	99		GLY					1	1	1(GLY)	
	100		GLY					1	1	1(GLY)	
	101		GLY					1	1	1(GLY)	
	102		THR					1	1	1(THR)	
F	103		LYS					1	1	1(LYS)	
R	104		LEU					1	1	1(LEU)	
4	105		THR					1	1	1(THR)	
	106		VAL					1	1	1(VAL)	
	106A		LEU					1	1	1(LEU)	
	107		GLY					1	1	1(GLY)	
	108		GLN					1	1	1(GLN)	
	109		PRO					1	1	1(PRO)	

REFERENCE: HUMAN LAMBDA LIGHT CHAINS SUBGROUP IV

1) **SH:** TITANI,K.,WIKLER,M.,SHINODA,T. & PUTNAM,F.W. (1970) J.BIOL.CHEM.,245,2171-2176. (CHECKED BY AUTHOR 06/15/83)

2) **NEV:** WANG,A.C.,WELLS,J.V.,FUDENBERG,H.H. & GERGELY,J. (1974) IMMUNOCHEM.,11,341-345. (CHECKED BY AUTHOR)

3) **USH:** TISCHENDORF,F.W.,TISCHENDORF,M.M. & WITTMANN-LIEBOLD,B. (1976) Z.NATURFORSCH,31C,758-760.

4) **PFA:** TISCHENDORF,F.W.,TISCHENDORF,M.M. & WITTMANN-LIEBOLD,B. (1976) Z.NATURFORSCH,31C,758-760.

5) **FRA':** WANG,A.C. & FUDENBERG,H.H. (1974) J.IMMUNOGENETICS,1,303-313. (CHECKED BY AUTHOR)

NOTES: HUMAN LAMBDA LIGHT CHAINS SUBGROUP IV

IDENTICAL SETS OF FRAMEWORK SEGMENTS:

FR1: SET 1: SH[1],NEV[2]. (2 IDENTICAL)

FR2:

FR3:

FR4: SET 1: SH[1]. (IDENTICAL TO 4 HUMAN V-LAMBDA-I: BL2 'CL[6],RHE[10],OKA[12],NIG-51[19]; 5 HUMAN V-LAMBDA-II: MES[2],ES492[8], TRO[14],VIL[17],WIN[21]; 4 HUMAN V-LAMBDA-III: HIL[1],CAP[4],BAU[12],DEL[14]; 3 HUMAN V-LAMBDA-VI: SUT[2],THO[4], LBV'CL[5]; AND 24 MOUSE V-LAMBDA: MOPC104E[1],J558[2],XS104[3],HOPC1[4],J698[5],H2061[6],W3159[7],Y5431[8],Y5485[9], Y5830[10],Y5669[11],MOPC511(L)[12],S178[13],Y5444[14],Y5606[15],S176[16],H2020[17],RPC20[18],IG 303LAMBDA'CL[19], S43'CL[21],S2H5'CL[38],S2E9'CL[39],S1F12'CL[40],IG 25LAMBDA'CL[41].)

+ THE FOLLOWING WERE EQUALLY AND MOST FREQUENTLY OCCURRING:

AT POSITION	RESIDUES
19	(VAL,ALA)
27	(LYS,SER)
30	(ALA,GLY,ASP,GLN)
32	(TYR,ASP,ASN)
34	(ILE,ALA,SER)

HUMAN LAMBDA LIGHT CHAINS SUBGROUP V

*		INVARIANT RESIDUES	1 BO	2 HBJ 2	3* MCG	# OF SEQUENCES	# OF AMINO ACIDS	OCCURRENCES OF MOST COMMON AMINO ACID	VARIABILITY
	0		---	---	---				
	1	PCA	PCA	PCA	PCA	3	1	3(PCA)	1.
	2	SER	SER	SER	SER	3	1	3(SER)	1.
	3	ALA	ALA	ALA	ALA	3	1	3(ALA)	1.
	4	LEU	LEU	LEU	LEU	3	1	3(LEU)	1.
	5	THR	THR	THR	THR	3	1	3(THR)	1.
	6	GLN	GLN	GLN	GLN	3	1	3(GLN)	1.
	7	PRO	PRO	PRO	PRO	3	1	3(PRO)	1.
	8	PRO	PRO	PRO	PRO	3	1	3(PRO)	1.
	9	SER	SER	SER	SER	3	1	3(SER)	1.
	10		---	---	---				
FR1	11	ALA	ALA	ALA	ALA	3	1	3(ALA)	1.
FR1	12	SER	SER	SER	SER	3	1	3(SER)	1.
FR1	13	GLY	GLY	GLY	GLY	3	1	3(GLY)	1.
FR1	14	SER	SER	SER	SER	3	1	3(SER)	1.
	15	-	PRO	PRO	leu	3	2	2(PRO)	3.
	16	GLY	GLY	GLY	GLY	3	1	3(GLY)	1.
	17	GLN	GLN	GLN	GLN	3	1	3(GLN)	1.
	18	SER	SER	SER	SER	3	1	3(SER)	1.
	19	VAL	VAL	VAL	VAL	3	1	3(VAL)	1.
	20	THR	THR	THR	THR	3	1	3(THR)	1.
	21	ILE	ILE	ILE	ILE	3	1	3(ILE)	1.
	22	SER	SER	SER	SER	3	1	3(SER)	1.
	23	CYS	CYS	CYS	CYS	3	1	3(CYS)	1.
	24	THR	THR	THR	THR	3	1	3(THR)	1.
	25	GLY	GLY	GLY	GLY	3	1	3(GLY)	1.
	26	THR	THR	THR	THR	3	1	3(THR)	1.
	27	SER	SER		SER	2	1	2(SER)	1.
	27A		---		---				
	27B		---		---				
	27C		---		---				
CDR1	27D	SER	SER		SER	2	1	2(SER)	
CDR1	27E	ASP	ASP		ASP	2	1	2(ASP)	
CDR1	27F	VAL	VAL		VAL	2	1	2(VAL)	
CDR1	28	GLY	GLY		GLY	2	1	2(GLY)	1.
	29		ASP		GLY	2	2	1(+)	4.
	30		ASN		TYR	2	2	1(+)	4.
	31		LYS		ASN	2	2	1(+)	4.
	32	TYR	TYR		TYR	2	1	2(TYR)	1.
	33	VAL	VAL		VAL	2	1	2(VAL)	1.
	34	SER	SER		SER	2	1	2(SER)	1.
	35	TRP	TRP		TRP	2	1	2(TRP)	1.
	36	TYR	TYR		TYR	2	1	2(TYR)	1.
	37	GLN	GLN		GLN	2	1	2(GLN)	1.
	38	GLN	GLN		GLN	2	1	2(GLN)	1.
	39	HIS	HIS		HIS	2	1	2(HIS)	1.
	40		PRO		ALA	2	2	1(+)	4.
FR2	41	GLY	GLY		GLY	2	1	2(GLY)	1.
FR2	42		ARG		LYS	2	2	1(+)	4.
FR2	43	ALA	ALA		ALA	2	1	2(ALA)	1.
	44	PRO	PRO		PRO	2	1	2(PRO)	1.
	45	LYS	LYS		LYS	2	1	2(LYS)	1.
	46		LEU		VAL	2	2	1(+)	4.
	47		VAL		ILE	2	2	1(+)	4.
	48	ILE	ILE		ILE	2	1	2(ILE)	1.
	49		PHE		TYR	2	2	1(+)	4.
	50	GLU	GLU		GLU	2	1	2(GLU)	1.
	51	VAL	VAL		VAL	2	1	2(VAL)	1.
CDR2	52		SER		ASN	2	2	1(+)	4.
CDR2	53		GLY		LYS	2	2	1(+)	4.
	54	ARG	ARG		ARG	2	1	2(ARG)	1.
	55	PRO	PRO		PRO	2	1	2(PRO)	1.
	56	SER	SER		SER	2	1	2(SER)	1.
	57	GLY	GLY		GLY	2	1	2(GLY)	1.
	58	VAL	VAL		VAL	2	1	2(VAL)	1.
	59	PRO	PRO		PRO	2	1	2(PRO)	1.
	60	ASP	ASP		ASP	2	1	2(ASP)	1.
	61	ARG	ARG		ARG	2	1	2(ARG)	1.
	62	PHE	PHE		PHE	2	1	2(PHE)	1.
	63	SER	SER		SER	2	1	2(SER)	1.
	64	GLY	GLY		GLY	2	1	2(GLY)	1.
	65	SER	SER		SER	2	1	2(SER)	1.
	66	LYS	LYS		LYS	2	1	2(LYS)	1.
	67	SER	SER		SER	2	1	2(SER)	1.
	68		ASP		GLY	2	2	1(+)	4.
	69	ASN	ASN		ASN	2	1	2(ASN)	1.
	70	THR	THR		THR	2	1	2(THR)	1.
	71	ALA	ALA		ALA	2	1	2(ALA)	1.
FR3	72	SER	SER		SER	2	1	2(SER)	1.
FR3	73	LEU	LEU		LEU	2	1	2(LEU)	1.
	74	THR	THR		THR	2	1	2(THR)	1.
	75	VAL	VAL		VAL	2	1	2(VAL)	1.
	76	SER	SER		SER	2	1	2(SER)	1.
	77	GLY	GLY		GLY	2	1	2(GLY)	1.
	78	LEU	LEU		LEU	2	1	2(LEU)	1.
	79		ARG		GLN	2	2	1(+)	4.
	80	ALA	ALA		ALA	2	1	2(ALA)	1.
	81	GLU	GLU		GLU	2	1	2(GLU)	1.
	82	ASP	ASP		ASP	2	1	2(ASP)	1.
	83	GLU	GLU		GLU	2	1	2(GLU)	1.
	84	ALA	ALA		ALA	2	1	2(ALA)	1.
	85	ASP	ASP		ASP	2	1	2(ASP)	1.
	86	TYR	TYR		TYR	2	1	2(TYR)	1.
	87	TYR	TYR		TYR	2	1	2(TYR)	1.
	88	CYS	CYS		CYS	2	1	2(CYS)	1.
	89	SER	SER		SER	2	1	2(SER)	1.
	90	SER	SER		SER	2	1	2(SER)	1.
	91	TYR	TYR		TYR	2	1	2(TYR)	1.
	92		VAL		GLU	2	2	1(+)	4.
	93		ASP		GLY	2	2	1(+)	4.
	94		ASN		SER	2	2	1(+)	4.
	95		ASN		ASP	2	2	1(+)	4.
CDR3	95A	ASN	ASN		ASN	2	1	2(ASN)	
CDR3	95B		---		---				
CDR3	95C		---		---				
CDR3	95D		---		---				
CDR3	95E		---		---				
CDR3	95F		---		---				
	96	PHE	PHE		PHE	2	1	2(PHE)	1.
	97	VAL	VAL		VAL	2	1	2(VAL)	1.
	98	PHE	PHE		PHE	2	1	2(PHE)	1.
	99	GLY	GLY		GLY	2	1	2(GLY)	1.
	100		GLY		THR	2	2	1(+)	4.
	101	GLY	GLY		GLY	2	1	2(GLY)	1.
FR4	102	THR	THR		THR	2	1	2(THR)	1.
FR4	103	LYS	LYS		LYS	2	1	2(LYS)	1.
FR4	104		LEU		VAL	2	2	1(+)	4.
FR4	105	THR	THR		THR	2	1	2(THR)	1.
FR4	106	VAL	VAL		VAL	2	1	2(VAL)	1.
FR4	106A	LEU	LEU		LEU	2	1	2(LEU)	
	107		ARG		GLY	2	2	1(+)	4.
	108	GLN	GLN		GLN	2	1	2(GLN)	1.
	109	PRO	PRO		PRO	2	1	2(PRO)	1.

ANTIBODY SPECIFICITIES: HUMAN LAMBDA LIGHT CHAINS SUBGROUP V

3) **MCG:** ANTI-EPSILON-DNP-LYS, EPSILON-DNP-AMINOCAPROATE, DNP-LEU, TRIACETIN, SODIUM MERTHIOLATE, METHADONE, 1,10-PHENANTHROLINE, CAFFEINE, THEOPHYLLINE, DI-DNP-LYS, DNP-TRP, DNP-PHE, DI-DNP-TYR, COLCHICINE, P-NITROANILINE, P-NITROPHENYLPHOSPHORYL CHOLINE, 5-ACETYLURACIL, MENADIONE, MEPERIDINE, TRIBUTYRIN, OMEGA-BROMOHEPTANOATE, O-CHLOROMERCURIPHENOL, P-CHLOROMERCURIPHENOL, PHENYLMERCURIC COMPOUNDS, METHYL-MERCURIC CHLORIDE.

REFERENCE: HUMAN LAMBDA LIGHT CHAINS SUBGROUP V

1) **BO:** WIKLER,M. & PUTNAM,F.W. (1970) J.BIOL.CHEM.,245,4488-4507. (CHECKED BY AUTHOR 06/15/83)

2) **HBJ2:** HOOD,L.,GRAY,W.R.,SANDERS,B.G. & DREYER,W.J. (1967) COLD SPRING HARBOR SYMP. QUANTITATIVE BIOL.,32,133-145.

3) **MCG:** FETT,J.W. & DEUTSCH,H.F. (1974) BIOCHEMISTRY,13,4102-4114. (CHECKED BY AUTHOR)

NOTES: HUMAN LAMBDA LIGHT CHAINS SUBGROUP V

IDENTICAL SETS OF FRAMEWORK SEGMENTS:

FR1: SET 1: BO[1],HBJ2[2]. (2 IDENTICAL)

FR2:

FR3: -

FR4: SET 1: BO[1]. (IDENTICAL TO 1 HUMAN V-LAMBDA-I: NEWM[1]; AND 1 HUMAN V-LAMBDA-II: WH[3].)
SET 2: MCG[3]. (IDENTICAL TO 1 HUMAN V-LAMBDA-I: LOC[11].)

IDENTICAL SETS OF COMPLEMENTARITY DETERMINING REGIONS:

CDR1: SET 1: MCG[3]. (IDENTICAL TO 2 HUMAN V-LAMBDA-II: MES[2],VIL[17].)

CDR2:

CDR3:

\+ THE FOLLOWING WERE EQUALLY AND MOST FREQUENTLY OCCURRING:

AT POSITION	RESIDUES
29	(GLY,ASP)
30	(TYR,ASN)
31	(LYS,ASN)
40	(PRO,ALA)
42	(LYS,ARG)
46	(LEU,VAL)
47	(ILE,VAL)
49	(TYR,PHE)
52	(SER,ASN)
53	(LYS,GLY)
68	(GLY,ASP)
79	(ARG,GLN)
92	(VAL,GLU)
93	(GLY,ASP)
94	(SER,ASN)
95	(ASP,ASN)
100	(THR,GLY)
104	(LEU,VAL)
107	(ARG,GLY)

HUMAN LAMBDA LIGHT CHAINS SUBGROUP VI

		INVARIANT RESIDUES	1 AMYLOID -AR #	2 SUT #	3 AMYLOID -RS	4 THO #	5 LBV CL #	6 GIO	7 YAM	8 WAN	9 WIN	10 NIG -48 #	11 JAM	12 MOR	13 KIN	# OF SEQUENCES	# OF AMINO ACIDS	OCCURRENCES OF MOST COMMON AMINO ACID	VARIABILITY
	0		---	---	---	---	---	---	---	---	---	---	---	---	---				
	1		ASP	ASP	ASP	asn	asn	asn	ASP	asn	asn	asn	ASP	asn	asn	13	2	8(ASN)	3.3
	2		PHE	PHE	PHE	PHE	PHE	PHE	PHE	PHE	PHE	leu	PHE	leu	PHE	13	2	11(PHE)	2.4
	3		MET	MET	MET	MET	MET	MET	MET	ile	MET	MET	MET	MET	MET	13	2	12(MET)	2.2
	4	LEU	LEU	LEU	LEU	LEU	LEU	LEU	LEU	LEU	LEU	LEU	LEU	LEU	LEU	13	1	13(LEU)	1.
	5		THR	THR	THR	THR	THR	THR	THR	THR	THR	ile	THR	THR	leu	13	3	11(THR)	3.5
	6		GLN	GLN	GLN	GLN	GLN	GLN	GLN	GLN	GLN	GLN	glu	GLN	GLN	13	2	12(GLN)	2.2
	7	PRO	PRO	PRO	PRO	PRO	PRO	PRO	PRO	PRO	PRO	PRO	PRO	PRO	PRO	13	1	13(PRO)	1.
	8		HIS	HIS	HIS	HIS	HIS	HIS	HIS			pro	HIS	HIS	HIS	11	2	10(HIS)	2.2
	9	SER	SER	SER	SER	SER	SER	SER	SER	SER	SER	SER	SER	SER	SER	13	1	13(SER)	1.
	10		---	---	---	---	---	---	---	---	---	---	---	---	---				
	11		VAL	VAL	VAL	VAL	VAL	VAL	VAL	VAL	VAL	VAL	VAL	leu	VAL	13	2	12(VAL)	2.2
	12	SER	SER	SER	SER	SER	SER	SER	SER	SER	SER	SER	SER	SER	SER	13	1	13(SER)	1.
	13		GLU	GLU	GLU	GLU	GLU	GLU	GLU	GLU	GLU	GLU	GLU	asp		12	2	11(GLU)	2.2
	14	SER	SER	SER	SER	SER	SER	SER	SER	SER		SER	SER	SER		11	1	11(SER)	1.
	15	PRO	PRO	PRO	PRO	PRO	PRO	PRO	PRO	PRO	PRO	PRO	PRO	PRO		12	1	12(PRO)	1.
	16	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY		12	1	12(GLY)	1.
	17		LYS	LYS	gln	LYS	LYS	LYS	gly	LYS	LYS	LYS	LYS	LYS		12	3	10(LYS)	3.6
	18		THR	THR	THR	THR	THR	THR	lys	THR	THR	THR		THR		11	2	10(THR)	2.2
	19		VAL	VAL	VAL	VAL	VAL	VAL	VAL	VAL	VAL	VAL		ile		11	2	10(VAL)	2.2
	20		THR	ile	THR	THR	THR	THR	ser	THR	THR	THR		ile		11	3	8(THR)	4.1
	21		PHE	ile	ile	ile	ile	ile	ile	ile		met		ile		10	3	8(ILE)	3.8
	22	SER	SER	SER	SER	SER	SER	SER	SER	SER		SER		SER		10	1	10(SER)	1.
	23	CYS	CYS	CYS	CYS	CYS	CYS	CYS	CYS			CYS		CYS		10	1	10(CYS)	1.
	24		THR	THR	THR	THR	THR	THR	SER			THR		THR		9	2	8(THR)	2.3
	25		GLY	ARG	GLY	ARG	GLY					ARG		ALA		7	3	3(-)	7.
	26		SER	SER	SER	SER	ASN					THR		ASN		7	3	4(SER)	5.3
	27		GLY	ASP	GLY	SER	SER					SER		GLY		7	3	3(-)	7.
	27A		GLY	GLY	ASP	GLY	GLY		ALA			---		GLY		7	3	5(GLY)	
	27B		SER	THR	SER	SER	SER					---		ASN		6	3	4(SER)	
	27C		---	---	---	---	---					---		---					
	27D		---	---	---	---	---					---		---					
	27E		---	---	---	---	---					ASP		---		1	1	1(ASP)	
	27F		---	---	---	---	---					SER		---		1	1	1(SER)	
	28	ILE	ILE	ILE	ILE	ILE	ILE					ILE		ILE		7	1	7(ILE)	1.
	29		ALA	ALA	ALA	ALA	ALA					ALA		GLY		7	2	6(ALA)	2.3
	30		ASP	GLY		SER	SER					SER		SER		6	3	4(SER)	4.5
	31		SER	TYR	SER	TYR	ASN					ASN		HIS		7	4	2(-)	14.
	32		PHE	TYR	TYR	TYR	TYR					TYR		PRO		7	3	5(TYR)	4.2
	33	VAL	VAL	VAL	VAL	VAL	VAL					VAL		VAL		7	1	7(VAL)	1.
	34	GLN	GLN	GLN		GLN	GLN					GLN				5	1	5(GLN)	1.
	35	TRP	TRP	TRP		TRP	TRP					TRP		TRP		6	1	6(TRP)	1.
	36	TYR	TYR	TYR		TYR	TYR					TYR		TYR		6	1	6(TYR)	1.
	37		GLN	GLN		GLN	GLN					ARG		LYS		6	3	4(GLN)	4.5
	38		GLN	GLN		LEU	GLN					GLN				5	2	4(GLN)	2.5
	39	ARG	ARG	ARG		ARG	ARG					ARG				5	1	5(ARG)	1.
	40		PRO	PRO		PRO	ARG					PRO		PRO		6	2	5(PRO)	2.4
	41		GLY	GLY		GLY	VAL					GLY		ASP		6	3	4(GLY)	4.5
	42		SER	ARG		SER	SER					GLY		SER		6	3	4(SER)	4.5
	43	ALA	ALA	ALA		ALA	ALA					ALA				5	1	5(ALA)	1.
	44	PRO	PRO	PRO		PRO	PRO					PRO				5	1	5(PRO)	1.
	45	THR	THR	THR		THR	THR					THR				5	1	5(THR)	1.
	46		THR	THR		THR	ILE					THR				5	2	4(THR)	2.5
	47		VAL	VAL		VAL	VAL					LEU				5	2	4(VAL)	2.5
	48	ILE	ILE	ILE		ILE	ILE					ILE				5	1	5(ILE)	1.
	49		TYR	PHE		TYR	TYR					TYR				5	2	4(TYR)	2.5
	50		ASP	GLU		GLU	GLU					ASP				5	2	3(GLU)	3.3
	51		ASP	ASP		ASP	ASP					THR				5	2	4(ASP)	2.5
	52		ASN	THR		ASN	ASN					ASN				5	2	4(ASN)	2.5
	53	GLN	GLN	GLN		GLN	GLN					GLN				5	1	5(GLN)	1.
	54	ARG	ARG	ARG		ARG	ARG					ARG				5	1	5(ARG)	1.
	55	PRO	PRO	PRO		PRO	PRO					PRO				5	1	5(PRO)	1.
	56		SER	SER		SER	LEU					TYR				5	3	3(SER)	5.
	57	GLY	GLY	GLY		GLY	GLY					GLY				5	1	5(GLY)	1.
	58	VAL	VAL	VAL		VAL	VAL					VAL				5	1	5(VAL)	1.
	59	PRO	PRO	PRO		PRO	PRO					PRO				5	1	5(PRO)	1.
	60		ASP	ASP		ASP	ASP					ASN				5	2	4(ASP)	2.5
	61	ARG	ARG	ARG		ARG	ARG					ARG				5	1	5(ARG)	1.
	62	PHE	PHE	PHE		PHE	PHE					PHE				5	1	5(PHE)	1.
	63	SER	SER	SER		SER	SER					SER				5	1	5(SER)	1.
	64	GLY	GLY	GLY		GLY	GLY					GLY				5	1	5(GLY)	1.
	65	SER	SER	SER		SER	SER					SER				5	1	5(SER)	1.
	66		#	#		#	#					#							
	67	SER	SER	SER		SER	SER					SER				5	1	5(SER)	1.
	68		ALA	SER		SER	SER					SER				5	2	4(SER)	2.5
	69	ASN	ASN	ASN		ASN	ASN					ASN				5	1	5(ASN)	1.
	70	SER	SER	SER		SER	SER					SER				5	1	5(SER)	1.
	71	ALA	ALA	ALA		ALA	ALA					ALA				5	1	5(ALA)	1.
	72	SER	SER	SER		SER	SER					SER				5	1	5(SER)	1.
	73	LEU	LEU	LEU		LEU	LEU					LEU				5	1	5(LEU)	1.
	74	THR	THR	THR		THR	THR					THR				5	1	5(THR)	1.
	75		ILE	ILE		VAL	ILE					ILE				5	2	4(ILE)	2.5
	76	SER	SER	SER		SER	SER					SER				5	1	5(SER)	1.
	77		GLY	GLY		GLU	GLY					GLY				5	2	4(GLY)	2.5
	78	LEU	LEU	LEU		LEU	LEU					LEU				5	1	5(LEU)	1.
	79		LYS	GLN		LYS	LYS					THR				5	3	3(LYS)	5.
	80		THR	THR		THR	THR					ASN				5	2	4(THR)	2.5
	81		GLU	GLU		GLU	GLU					ASP				5	2	4(GLU)	2.5
	82	ASP	ASP	ASP		ASP	ASP					ASP				5	1	5(ASP)	1.
	83		GLU	GLU		GLU	GLU					THR				5	2	4(GLU)	2.5
	84	ALA	ALA	ALA		ALA	ALA					ALA				5	1	5(ALA)	1.
	85		ASP	ASP		ASP	ASP					MET				5	2	4(ASP)	2.5
	86	TYR	TYR	TYR		TYR	TYR					TYR				5	1	5(TYR)	1.
	87		TYR	TYR		TYR	TYR					PHE				5	2	4(TYR)	2.5
	88	CYS	CYS	CYS		CYS	CYS					CYS				5	1	5(CYS)	1.
	89	GLN	GLN	GLN		GLN	GLN					GLN				5	1	5(GLN)	1.
	90	SER	SER	SER		SER	SER					SER				5	1	5(SER)	1.
	91		TYR	TYR		TYR	PHE					TYR				5	2	4(TYR)	2.5
	92		ASN	ASP		ASP	ASP					ASP				5	2	4(ASP)	2.5
	93		SER	ARG		SER	ASN					SER				5	3	3(SER)	5.
	94		ASN	ASP		ASN	THR					SER				5	4	2(ASN)	10.
	95		HIS	HIS		ASN	ASN					ASN				5	2	3(ASN)	3.3
	95A		HIS	---		---	GLN					LEU				3	3	1(-)	
	95B		---	---		---	---					---							
	95C		---	---		---	---					---							
	95D		---	---		---	---					---							
	95E		---	---		---	---					---							
	95F		---	---		---	---					---							
	96		VAL	TRP		TRP	GLY					TRP				5	3	3(TRP)	5.
	97	VAL	VAL	VAL		VAL	VAL					VAL				5	1	5(VAL)	1.
	98	PHE	PHE	PHE		PHE	PHE					PHE				5	1	5(PHE)	1.
	99	GLY	GLY	GLY		GLY	GLY					GLY				5	1	5(GLY)	1.
	100	GLY	GLY	GLY		GLY	GLY					GLY				5	1	5(GLY)	1.
	101	GLY	GLY	GLY		GLY	GLY					GLY				5	1	5(GLY)	1.
	102	THR	THR	THR		THR	THR					THR				5	1	5(THR)	1.
	103	LYS	LYS	LYS		LYS	LYS					LYS				5	1	5(LY3)	1.
	104		VAL	LEU		LEU	LEU					LEU		LEU		6	2	5(LEU)	2.4
	105	THR	THR	THR		THR	THR					THR		THR		6	1	6(THR)	1.
	106	VAL	VAL	VAL		VAL	VAL					VAL		VAL		6	1	6(VAL)	1.
	106A	LEU	LEU	LEU		LEU	LEU					LEU		LEU		6	1	6(LEU)	
	107		GLY	GLY		GLY	GLY					SER		SER		6	2	4(GLY)	3.
	108	GLN	GLN	GLN		GLN	GLN					GLN		GLN		6	1	6(GLN)	1.
	109	PRO	PRO	PRO		PRO	PRO					PRO		PRO		6	1	6(PRO)	1.

HUMAN HEAVY CHAINS SUBGROUP I

		INVARIANT RESIDUES	1 EU	2* SIE	3 HG3 'CL #	4* WOL	5 CA	6 ND 'CL #	7 MOT #	8 BRO 'IGG	9 THO	10* STE	11 BEN (I)	12 ZUC #	13 DI	14 BOT #	15 OMM 'CL #	16* MAR	17 FI	18 VU	19 WAR	20 VIL	21 DUN	22 ADA	23 NOR	24 SAW
	0		---	---	#	---	---	---	---	---	---	---	---	---	---	---	---	---	---	---	---	---	---	---	---	---
	1		PCA	PCA	gln	PCA	PCA	gln	PCA	glu	glu	PCA	glu	PCA	PCA	asp	gln	PCA	PCA	PCA	PCA	PCA	PCA	PCA	PCA	PCA
	2		VAL	VAL	VAL	VAL	VAL	thr	VAL	VAL	VAL	VAL	leu	VAL	VAL	ser	VAL	GLN	GLN	GLN	GLN	GLN	GLN	GLN	GLN	VAL
	3		GLN	GLN	GLN	GLN	GLN	GLN	GLN	GLN	GLN	his	GLN	GLN	GLN	pro	his	LEU	LEU	LEU	LEU	LEU	LEU			glu
	4	LEU(.96)	LEU	LEU	LEU	LEU	LEU	LEU	LEU	LEU	LEU	LEU	LEU	val	LEU	LEU	LEU										LEU
	5		VAL	VAL	VAL	met	VAL	VAL	VAL	VAL	VAL	VAL	VAL	VAL		glu	gln									
	6		GLN	GLN	GLN	GLN	glu	GLN	GLN	GLN	GLN	glu	GLN	glu		GLN	glu									
	7	SER	SER	SER	SER	SER	SER	SER	SER	SER	SER	SER	SER	SER		SER	SER									
	8		GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	ser	GLY	GLY	GLY	GLY	GLY									
	9		ALA	ALA	ALA	ALA	ALA	ALA	ALA	ALA	ALA	ALA	ALA	ALA	gly	his	pro									
	10		GLU	GLU	GLU	GLU	GLU	GLU	GLU	GLU	GLU	GLU	GLU	asp		GLU	gly									
	11		VAL	VAL	VAL	VAL	VAL	VAL	VAL	VAL	VAL	VAL	VAL	leu		VAL	leu									
	12		LYS	LYS	LYS	LYS	arg	arg	LYS	LYS	LYS	LYS	ser	val	LYS	gly	gly									
	13		LYS	LYS	LYS	LYS	LYS	LYS	LYS	LYS	LYS	LYS		LYS	LYS	ile	LYS									
FR1	14		PRO	PRO	PRO	PRO	PRO	PRO	PRO	PRO	PRO	PRO	PRO	PRO		leu	PRO									
	15		GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY		lys	pro									
	16		SER	SER	ala	SER	ala	ala	SER	glu	glu	ala		gly		glu	---									
	17		SER	SER	SER	SER	SER	SER	SER	SER	SER	SER		---		thr	---									
	18		VAL	VAL	VAL	VAL	VAL	VAL	ala	leu	leu	met		---		glu	---									
	19		LYS	arg	LYS	arg	LYS	arg	arg	LYS	arg	LYS		---	LYS	ala	---									
	20		VAL	VAL	VAL	VAL	ile	VAL	leu	ile	ile	VAL		---		glu	---									
	21		SER	thr	SER	SER	SER	SER	SER	SER	SER	SER		---		asp	---									
	22		CYS	CYS	CYS	CYS	CYS	CYS	CYS			CYS		---		arg	---									
	23		LYS	LYS	LYS	LYS	LYS	LYS	LYS	LYS	LYS	arg		---		ile	---									
	24		ALA	thr	ALA	thr	thr	ALA	val	gly	gly	ALA		---		ile	---									
	25		SER	SER	SER	SER	SER	SER	SER	SER	phe			---		lys	---									
	26		GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY			---		glu	---									
	27		GLY	GLY	tyr	GLY	tyr	tyr	asp	tyr	tyr			---		glu	---									
	28		THR	THR	THR	THR	THR	THR	asp					---		glu	---									
	29		PHE	PHE	PHE	PHE	PHE	PHE	PHE					---		ala	---									
	30		SER	SER	asn	val	SER	ile	asn					---		arg	---									
	31		ARG	GLY	SER	ASP	HIS	ASP	THR					---		LEU	---									
	32		SER	TYR	TYR	TYR	TYR	SER	TYR					---		SER	---									
CDR	33		ALA	THR	TYR	LYS	ALA	TYR	ASP					---		GLY	---									
	34		ILE	ILE	MET	GLY	MET	ILE	ILE					---		ARG	---									
1	35		ILE	SER	HIS	LEU		HIS	HIS					---	SER	ASP	---									
	35A		---	---	---	---		---	---					---	---	---	---									
	35B		---	---	---	---		---	---					---	---	---	---									
	36		TRP	TRP	TRP	TRP		TRP	TRP					---	TRP	MET	---									
	37		VAL	VAL	VAL	VAL		ILE	VAL					---	ILE	GLN	---									
	38		ARG	ARG	ARG	ARG		ARG	ARG					---	ARG	VAL	---									
	39		GLN	GLN	GLN	GLN		GLN	GLN					---	GLN	THR	---									
	40		ALA	ALA	ALA	ALA		ALA	ALA					---	PRO	SER	---									
	41		PRO	PRO	PRO	PRO		PRO	PRO					---	PRO	GLN	---									
FR2	42		GLY	GLY	GLY	GLY		GLY	GLY					---	GLY	PRO	---									
	43		GLN	ARG	GLN	LYS		HIS	ARG					---	LYS	---	---									
	44	GLY	GLY	GLY	GLY	GLY		GLY	GLY					---	GLY	---	---									
	45	LEU	LEU	LEU	LEU	LEU		LEU	LEU					---	LEU	---	---									
	46	GLU	GLU	GLU	GLU	GLU		GLU	GLU					---	GLU	---	---									
	47	TRP	TRP	TRP	TRP	TRP		TRP	TRP					---	TRP	---	---									
	48		MET	VAL	MET	VAL		VAL	MET					---	VAL	---	---									
	49		GLY	GLY	GLY	GLY		GLY	ALA					---	GLY	---	---									
	50		GLY	SER	ILE	GLN		TRP	VAL					---	GLU	---	---									
	51		ILE	PRO	ILE	ILE		ILE	VAL					---	ILE	---	---									
	52		VAL	ALA	ASN	PRO		ASN	HIS					---	ASP	---	---									
	52A		PRO	LYS	PRO	LEU		PRO	PRO					---	---	---	---									
	52B		---	---	---	---		---	---					---	---	---	---									
	52C		---	---	---	---		---	---					---	---	---	---									
	53		MET	TRP	SER	ARG		ASN	SER					---	TYR	---	---									
	54		PHE	THR	GLY	PHE		SER	ASP					---	SER	---	---									
CDR	55		GLY	ASP	GLY	ASN		GLY	ASP					---	GLY	---	---									
	56		PRO	PRO	SER	GLY		GLY	ARG					---	THR	---	---									
	57		PRO	PHE	THR	GLU		THR	THR					---	THR	---	---									
2	58		ASN	GLN	SER	VAL		ASN	THR					---	ASP	---	---									
	59		TYR	GLY	TYR	LYS		TYR	TYR					---	TYR	---	---									
	60		ALA	VAL	ALA	ASN		ALA	GLY					---		---	---									
	61		GLN	TYR	GLN	PRO		PRO	PRO					---		---	---									
	62		LYS	ILE	LYS	GLY		ARG	ARG					---		---	---									
	63		PHE	LYS	PHE	SER		PHE	SER					---		---	---									
	64		GLN	TRP	GLN	VAL		GLN	GLN					---	LYS	---	---									
	65		GLY	GLU	GLY	VAL		GLY	ALA					---	SER	---	---									
	66	ARG	ARG	ARG	ARG	ARG		ARG	ARG					---	ARG	---	---									
	67		VAL	VAL	VAL	VAL		VAL	PHE					---		---	---									
	68		THR	THR	THR	SER		THR	THR					---		---	---									
	69		ILE	VAL	MET	VAL		MET	VAL					---	MET	---	---									
	70		THR	SER	THR	SER		THR	THR					---	SER	---	---									
	71		ALA	LEU	ARG	LEU		ARG	ARG					---	LEU	---	---									
	72		ASP	LYS	ASP	LYS		ASP	ASP					---	ASP	---	---									
	73		GLU	PRO	THR	PRO		ALA	SER					---	THR	---	---									
	74	SER	SER	SER	SER	SER		SER	SER					---	SER	---	---									
	75		THR	PHE	THR	PHE		PHE	THR					---	VAL	---	---									
	76		ASN	ASN	SER	ASN		SER	THR					---	ASN	---	---									
	77		THR	GLN	THR	GLN		THR	THR					---	LEU	---	---									
	78		ALA	ALA	VAL	ALA		ALA	VAL					---	PHE	---	---									
	79		TYR	TYR	TYR	HIS		TYR	TYR					---	SER	---	---									
FR3	80		MET	MET	MET	MET		MET	MET					---	LEU	---	---									
	81		GLU	GLU	GLU	GLU		ASP	GLU					---	SER	---	---									
	82		LEU	LEU	LEU	LEU		LEU	LEU					---	LEU	---	---									
	82A		SER	VAL	SER	SER		ARG	THR					---	THR	---	---									
	82B		SER	ASN	SER	SER		SER	ALA					---	SER	---	---									
	82C		LEU	LEU	LEU	LEU		LEU	LEU					---	VAL	---	---									
	83		ARG	PHE	ARG	PHE		ARG	ILE					---	THR	---	---									
	84		SER	ASN	SER	SER		SER	SER					---	ALA	---	---									
	85		GLU	GLU	GLU	GLU		ASP	ALA					---	ALA	---	---									
	86		ASP	ASP	ASP	ASP		ASP	ASP					---	ASP	---	---									
	87		THR	GLY	THR	THR		SER	THR					---	THR	---	---									
	88	ALA	ALA	ALA	ALA	ALA		ALA	ALA					---	ALA	---	---									
	89		PHE	VAL	VAL	VAL		VAL	ILE					---	VAL	---	---									
	90		TYR	TYR	TYR	TYR		PHE	TYR					---	TYR	---	---									
	91		PHE	TYR	TYR	TYR		TYR	TYR					---	TYR	---	---									
	92	CYS	CYS	CYS	CYS	CYS		CYS	CYS					---	CYS	---	---									
	93		ALA	ALA	ALA	ALA		ALA	ALA					---	ALA	---	---									
	94		GLY	ARG	ARG	ARG		LYS	ARG					---	ARG	---	---									
	95		GLY	GLU	#	GLU		SER	GLY					---		---	---									
	96		TYR	TRP	---	TYR		ASP	ALA					---		---	---									
	97		GLY	LYS	---	GLY		PRO	HIS					---		---	---									
	98		ILE	GLY	---	PHE		PHE	TYR					---		---	---									
	99		TYR	GLN	---	ASP		TRP	SER					---		---	---									
	100		SER	VAL	---	THR		SER	ASP					---		---	---									
	100A		---	ASN	---	SER		ASP	THR					---		---	---									
CDR	100B		---	VAL	---	ASP		TYR	ASP					---		---	---									
	100C		---	ASN	---	TYR		TYR	ASP					---		---	---									
	100D		---	PRO	---	TYR		ASN	SER					---		---	---									
3	100E		---	---	---	---		PHE	GLY					---		---	---									
	100F		---	---	---	---		ASP	THR					---		---	---									
	100G		---	---	---	---		TYR	SER					---		---	---									
	100H		---	---	---	---		SER	LEU					---		---	---									
	100I		---	---	---	---		TYR	---					---		---	---									
	100J		---	---	---	---		THR	---					---		---	---									
	100K		---	PHE	---	TYR		LEU	---					---		---	---									
	101		PRO	ASP	---	TYR		ASP	GLY					---		---	---									
	102		GLU	TYR	---	TYR		VAL	PRO					---	ARG	---	---									
	103		GLU	TRP	---	TRP		TRP	TRP					---	TRP	---	---									
	104		TYR	GLY	---	GLY		GLY	GLY					---	GLY	---	---									
	105		ASN	GLN	---	GLN		GLN	GLN					---	SER	---	---									
	106	GLY	GLY	GLY	---	GLY		GLY	GLY					---	GLY	---	---									
FR	107		GLY	VAL	---	THR		THR	THR					---	GLY	---	---									
	108		LEU	LEU	---	LEU		THR	LEU					---	LEU	---	---									
4	109		VAL	VAL	---	VAL		VAL	LEU					---	VAL	---	---									
	110		THR	THR	---	THR		[illegible]	ILE					---	THR	---	---									
	111	VAL	VAL	VAL	---	VAL		VAL	VAL					---	VAL	---	---									
	112		SER	SER	---	SER		SER	SER					SER	SER	---	---									
	113	SER	SER	SER	---	SER		SER	SER					SER	SER	---	---									

HUMAN HEAVY CHAINS SUBGROUP I (cont'd)

		25* KOH	26 RIC	27 WIS #	28 VAU #	29 LEB #	30 SAC #	31 DEE	32 LEA	33 HAR	34 HUS	# OF SEQUENCES	# OF AMINO ACIDS	OCCURRENCES OF MOST COMMON AMINO ACID	VARIABILITY
	0	—	—	---	---	---	---		---	---					
	1	gln	PCA	PCA	PCA	PCA	gly		---	---		30	5	21(PCA)	7.1
	2	VAL	VAL	met	VAL	VAL	ala		---	---		30	6	25(VAL)	7.2
	3	GLN	leu	GLN	---	---	---		pca	pca		29	6	22(GLN)	7.9
	4	LEU		---	---	---	---		LEU	LEU		25	2	24(LEU)	2.1
	5			---	---	---	---					14	4	11(VAL)	5.1
	6			---	---	---	---					14	2	10(GLN)	2.8
	7			---	---	---	---					14	1	14(SER)	1.
	8			---	---	---	---					15	2	14(GLY)	2.1
	9			---	---	---	---					15	4	12(ALA)	5.
	10			---	---	---	---					14	3	12(GLU)	3.5
	11			---	---	---	---					14	2	12(VAL)	2.3
	12			---	---	---	---					15	5	9(LYS)	8.3
	13			---	---	---	---					14	2	13(LYS)	2.2
FR1	14			---	---	---	---					14	2	13(PRO)	2.2
	15			---	---	---	---					14	3	12(GLY)	3.5
	16			---	---	---	---					12	4	4(+)	12.
	17			---	---	---	---					11	2	10(SER)	2.2
	18			---	---	---	---	VAL				12	5	7(VAL)	8.6
	19			---	---	---	---	arg				13	3	6(+)	6.5
	20			---	---	---	---	ile				12	4	6(VAL)	8.
	21			---	---	---	---					11	3	9(SER)	3.7
	22			---	---	---	---					9	2	8(CYS)	2.3
	23			---	---	---	---					11	3	9(LYS)	3.7
	24			---	---	---	---					11	5	4(ALA)	14.
	25			---	---	---	---					10	3	8(SER)	3.8
	26			---	---	---	---					10	2	9(GLY)	2.2
	27			---	---	---	---					10	4	5(TYR)	8.
	28			---	---	---	---					8	3	6(THR)	4.
	29			---	---	---	---					8	2	7(PHE)	2.3
	30			---	---	---	---					8	5	3(SER)	13.
	31			---	---	---	---					8	7	2(ASP)	28.
	32			---	---	---	---					8	2	5(TYR)	3.2
	33			---	---	---	---					8	6	2(+)	24.
	34			---	---	---	---					8	4	4(ILE)	8.
CDR1	35			---	---	---	---					8	5	3(HIS)	13.
	35A			---	---	---	---								
	35B			---	---	---	---								
	36			---	---	---	---					8	2	7(TRP)	2.3
	37			---	---	---	---					8	3	5(VAL)	4.8
	38			---	---	---	---					8	2	7(ARG)	2.3
	39			---	---	---	---					8	2	7(GLN)	2.3
	40			---	---	---	---					8	3	6(ALA)	4.
	41			---	---	---	---					8	2	7(PRO)	2.3
FR2	42			---	---	---	---					8	2	7(GLY)	2.3
	43			---	---	---	---					7	4	2(+)	14.
	44			---	---	---	---					7	1	7(GLY)	1.
	45			---	---	---	---					7	1	7(LEU)	1.
	46			---	---	---	---					7	1	7(GLU)	1.
	47			---	---	---	---					7	1	7(TRP)	1.
	48			---	---	---	---					7	2	4(VAL)	3.5
	49			---	---	---	---					7	2	6(GLY)	2.3
	50			---	---	---	---					7	7	1(+)	49.
	51			---	---	---	---					7	3	5(ILE)	4.2
	52			---	---	---	---					7	6	2(ASN)	21.
	52A			---	---	---	---					6	3	4(PRO)	
	52B			---	---	---	---								
	52C			---	---	---	---								
	53			---	---	---	---					7	6	2(SER)	21.
	54			---	---	---	---					7	5	2(+)	18.
CDR2	55			---	---	---	---					7	3	4(GLY)	5.3
	56			---	---	---	---					7	5	2(+)	18.
	57			---	---	---	---					7	4	4(THR)	7.
	58			---	---	---	---					7	6	2(ASN)	21.
	59			---	---	---	---					7	3	5(TYR)	4.2
	60			---	---	---	---					6	4	3(ALA)	8.
	61			---	---	---	---					6	3	3(PRO)	6.
	62			---	---	---	---					6	4	2(+)	12.
	63			---	---	---	---					6	3	3(PHE)	6.
	64			---	---	---	---					7	4	4(GLN)	7.
	65			---	---	---	---					7	5	3(GLY)	12.
	66			---	---	---	---					7	1	7(ARG)	1.
	67			---	---	---	---					6	2	5(VAL)	2.4
	68			---	---	---	---					6	2	5(THR)	2.4
	69			---	---	---	---					7	3	3(+)	7.
	70			---	---	---	---					7	2	4(THR)	3.5
	71			---	---	---	---					7	3	3(+)	7.
	72			---	---	---	---					7	2	5(ASP)	2.8
	73			---	---	---	---					7	5	2(+)	18.
	74			---	---	---	---					7	1	7(SER)	1.
	75			---	---	---	---					7	3	3(+)	7.
	76			---	---	---	---					7	3	4(ASN)	5.3
	77			---	---	---	---					7	3	4(THR)	5.3
	78			---	---	---	---					7	3	4(ALA)	5.3
	79			---	---	---	---					7	3	5(TYR)	4.2
	80			---	---	---	---					7	2	6(MET)	2.3
	81			---	---	---	---					7	3	5(GLU)	4.2
FR3	82			---	---	---	---				MET	8	2	7(LEU)	2.3
	82A			---	---	---	---				ASN	8	5	3(SER)	
	82B			---	---	---	---				SER	8	3	6(SER)	
	82C			---	---	---	---				LEU	8	2	7(LEU)	
	83			---	---	---	---				ARG	8	4	4(ARG)	8.
	84			---	---	---	---				VAL	8	4	5(SER)	6.4
	85			---	---	---	---				GLX	8	3 : 4	5(GLU) : 4(GLU)	4.8 : 8.
	86			---	---	---	---				ASX	8	1 : 2	8(ASP) : 7(ASP)	1. : 2.3
	87			---	---	---	---				THR	8	3	6(THR)	4.
	88			---	---	---	---				ALA	8	1	8(ALA)	1.
	89			---	---	---	---				VAL	8	3	6(VAL)	4.
	90			---	---	---	---	TYR			TYR	9	2	8(TYR)	2.3
	91			---	---	---	---	TYR			TYR	9	2	8(TYR)	2.3
	92			---	---	---	---	CYS			CYS	9	1	9(CYS)	1.
	93			---	---	---	---	THR			ALA	9	2	8(ALA)	2.3
	94			---	---	---	---	GLY			ARG	9	3	6(ARG)	4.5
	95			---	---	---	---	ARG			ASX	7	5	2(+)	18.
	96			---	---	---	---	GLY			ARG	7	6	2(TYR)	21.
	97			---	---	---	---	MET			ASX	7	6	2(GLY)	21.
	98			---	---	---	---				ASX	6	5	2(PHE)	15.
	99			---	---	---	---				TYR	6	5	2(TYR)	15.
	100			---	---	---	---				GLY	6	5	2(SER)	15.
	100A			---	---	---	---				ASX	5	4	2(ASN) : 2(ASP)	
	100B			---	---	---	---				PHE	5	4	2(ASP)	
	100C			---	---	---	---				---	4	3	2(TYR)	
CDR3	100D			---	---	---	---				---	4	4	1(+)	
	100E			---	---	---	---				---	2	2	1(+)	
	100F			---	---	---	---				---	2	2	1(+)	
	100G			---	---	---	---				---	2	2	1(+)	
	100H			---	---	---	---				---	2	2	1(+)	
	100I			---	---	---	---				---	1	1	1(TYR)	
	100J			---	---	---	---				---	1	1	1(THR)	
	100K			---	---	---	---				---	3	3	1(+)	
	101			---	---	---	---	PRO			ASX	7	4 : 5	3(ASP) : 2(+)	9.3 : 18.
	102			---	---	---	---	GLX			TYR	8	5 : 6	3(TYR)	13. : 16.
	103			---	---	---	---	GLX			TRP	8	2 : 3	6(TRP)	2.7 : 4.
	104			---	---	---	---	THR			GLY	8	3	6(GLY)	4.
	105			---	---	---	---	ASX			GLX	8	3 : 5	5(GLN) : 4(GLN)	4.8 : 10.
	106		GLY	---	---	---					GLY	8	1	8(GLY)	1.
	107		VAL	---	---	LEU					THR	9	4	4(THR)	9.
FR	108		#	---	---	VAL					LEU	8	3	6(LEU)	4.
4	109		#	---	---	ILE					VAL	8	3	6(VAL)	4.
	110		THR	---	---	THR					THR	9	2	8(THR)	2.3
	111		VAL	---	---	VAL					VAL	9	1	9(VAL)	1.
	112		SER	---	---	SER					THR	10	2	9(SER)	2.2
	113		SER	---	---	SER					SER	10	1	10(SER)	1.

ANTIBODY SPECIFICITIES: HUMAN HEAVY CHAINS SUBGROUP I

2) **SIE:** ANTI-HUMAN GAMMA G GLOBULIN; WA IDIOTYPE
4) **WOL:** ANTI-HUMAN GAMMA G GLOBULIN; WA IDIOTYPE
10) **STE:** COLD AGGLUTININ WITH ANTI-BLOOD GROUP I ACTIVITY
16) **MAR:** ANTI-LIPOPROTEIN LIPASE
25) **KOH:** ANTI-HUMAN GAMMA G GLOBULIN

CLASS: HUMAN HEAVY CHAINS SUBGROUP I

1) **EU:** IGG1-KAPPA
2) **SIE:** IGM-KAPPA
4) **WOL:** IGM-KAPPA
5) **CA:** IGG1-
6) **ND'CL:** IGE-
7) **MOT:** IGG-
8) **BRO'IGG:** IGG-KAPPA
10) **STE:** IGG1-
11) **BEN(I):** IGG3-
12) **ZUC:** IGG3-
13) **DI:** IGM-
14) **BOT:** IGM-
15) **OMM'CL:** IGG3-
16) **MAR:** IGM-
19) **WAR:** IGG1-
20) **VIL:** IGG3-LAMBDA
21) **DUN:** IGG4-
22) **ADA:** IGA-
23) **NOR:** IGA-
24) **SAW:** IGG2-
25) **KOH:** IGM-LAMBDA
26) **RIC:** IGG3-
27) **WIS:** IGG3-
28) **VAU:** IGG1-
29) **LEB:** IGG1-
30) **SAC:** IGG1-KAPPA
34) **HUS:** IGG3-

REFERENCE: HUMAN HEAVY CHAINS SUBGROUP I

1) **EU:** CUNNINGHAM,B.A.,RUTISHAUSER,U.,GALL,W.E.,GOTTLIEB,P.D.,WAXDAL,M.J. & EDELMAN,G.M. (1970) BIOCHEMISTRY,9,3161-3170. (CHECKED BY AUTHOR)
2) **SIE:** ANDREWS,D.W. & CAPRA,J.D. (1981) PROC.NAT.ACAD.SCI.USA,78,3799-3803; ANDREWS,D.W. & CAPRA,J.D. (1981) BIOCHEMISTRY,20,5816-5822. (CHECKED BY AUTHOR 11/15/82); ANDREWS,D.W. & CAPRA,J.D. (1981) BIOCHEMISTRY,20,5822-5830.
3) **HG3'CL:** RECHAVI,G.,RAM.,D.,GLAZER,L.,ZAKUT,R. & GIVOL,D. (1983) PROC.NAT.ACAD.SCI.USA,80,855-859. (CHECKED BY AUTHOR 01/04/83)
4) **WOL:** ANDREWS,D.W. & CAPRA,J.D. (1981) PROC.NAT.ACAD.SCI.USA,78,3799-3803; ANDREWS,D.W. & CAPRA,J.D. (1981) BIOCHEMISTRY,20,5816-5822. (CHECKED BY AUTHOR 11/15/82); ANDREWS,D.W. & CAPRA,J.D. (1981) BIOCHEMISTRY,20,5822-5830.
5) **CA:** PITCHER,S.E. & KONIGSBERG,W. (1970) J.BIOL.CHEM.,245,1267-1274. (CHECKED BY AUTHOR)
6) **ND'CL:** BENNICH,H. & VON BAHR-LINDSTROM,H. (1974) PROGRESS IN IMMUNOLOGY,1,49-58; BENNICH,H.H.,JOHANSSON,S.G.O. & VON BAHR-LINDSTROM,H. (1978) IN IMMEDIATE HYPERSENSITIVITY: MODERN CONCEPTS AND DEVELOPMENTS, BACH,M.K., ED.,PP.1-36, MARCEL DEKKER,NEW YORK; KENTEN,J.H.,MOLGAARD,H.V.,HOUGHTON,M.,DERBYSHIRE,R.B.,VINEY,J.,BELL,L.O. & GOULD,H.J. (1982) PROC.NAT.ACAD.SCI.USA,79,6661-6665.
7) **MOT:** KOJIMA,M.,ODANI,S. & ONO,T. (1982) MOL.IMMUNOL.,19,1095-1103; KOJIMA,M.,KOIDE,T.,ODANI,S. & ONO,T. (1986) MOL.IMMUNOL.,23,169-174. (CHECKED BY AUTHOR 08/08/86)
8) **BRO'IGG:** HOPPER,J.E.,NOYES,C.,HEINRIKSON,R. & KESSEL,J.W. (1976) J.IMMUNOL.,116,743-746; HOPPER,J.E. & BRAHN,E. (1977) J.IMMUNOL.,119, 847-849. (CHECKED BY AUTHOR 08/25/78 WHO POINTED OUT THAT BRO' IS SAME AS BRIGG AND SUGGESTED THAT IT SHOULD BE RENAMED AS BROIGG)
9) **THO:** HOPPER,J.E. & BRAHN,E. (1977) J.IMMUNOL.,119,847-849. (CHECKED BY AUTHOR 08/25/78)
10) **STE:** FISHER,C.E.,PALM,W.H. & PRESS,E.M. (1969) FEBS LETTERS,5,20-22. (CHECKED BY AUTHOR)
11) **BEN(I):** KAPLAN,A.P.,HOOD,L.,TERRY,W.D. & METZGER,H. (1971) IMMUNOCHEMISTRY,8,801-811. (CHECKED BY AUTHOR)
12) **ZUC:** FRANGIONE,B. & MILSTEIN,C. (1969) NATURE,224,597-599. (CHECKED BY AUTHOR)
13) **DI:** KOHLER,H.,SHIMIZU,A.,PAUL,C.,MOORE,V. & PUTNAM,F.W. (1970) NATURE,227,1318-1320; FLORENT,G.,LEHMAN,D. & PUTNAM,F.W. (1974) BIOCHEMISTRY,13,2482-2498. (CHECKED BY AUTHOR 06/15/83)
14) **BOT:** BARNIKOL-WATANABE,S.,MIHAESCO,E.,MIHAESCO,C.,BARNIKOL,H.U. & HILSCHMANN,N. (1984) Z.PHYSIOL.CHEM.,365,105-118.
15) **OMM'CL:** ALEXANDER,A.,STEINMETZ,M.,BARRITAULT,D.,FRANGIONE,B.,FRANKLIN,E.C.,HOOD,L. & BUXBAUM,J.N. (1982) PROC.NAT.ACAD.SCI.USA,79, 3260-3264. (CHECKED BY AUTHOR 06/17/83)
16) **MAR:** KAPLAN,A.P.,HOOD,L.,TERRY,W.D. & METZGER,H. (1971) IMMUNOCHEMISTRY,8,801-811. (CHECKED BY AUTHOR)
17) **FI:** MONTGOMERY,P.C.,BELLO,A.C. & ROCKEY,J.H. (1970) BIOCHIM.BIOPHYS.ACTA,200,258-266. (CHECKED BY AUTHOR)
18) **VU:** MONTGOMERY,P.C.,BELLO,A.C. & ROCKEY,J.H. (1970) BIOCHIM.BIOPHYS.ACTA,200,258-266. (CHECKED BY AUTHOR)
19) **WAR:** KAPLAN,A.P.,HOOD,L.,TERRY,W.D. & METZGER,H. (1971) IMMUNOCHEMISTRY,8,801-811. (CHECKED BY AUTHOR)
20) **VIL:** KAPLAN,A.P.,HOOD,L.,TERRY,W.D. & METZGER,H. (1971) IMMUNOCHEMISTRY,8,801-811. (CHECKED BY AUTHOR)
21) **DUN:** KAPLAN,A.P.,HOOD,L.,TERRY,W.D. & METZGER,H. (1971) IMMUNOCHEMISTRY,8,801-811. (CHECKED BY AUTHOR)
22) **ADA:** KAPLAN,A.P.,HOOD,L.,TERRY,W.D. & METZGER,H. (1971) IMMUNOCHEMISTRY,8,801-811. (CHECKED BY AUTHOR)
23) **NOR:** KAPLAN,A.P.,HOOD,L.,TERRY,W.D. & METZGER,H. (1971) IMMUNOCHEMISTRY,8,801-811. (CHECKED BY AUTHOR)
24) **SAW:** KAPLAN,A.P.,HOOD,L.,TERRY,W.D. & METZGER,H. (1971) IMMUNOCHEMISTRY,8,801-811. (CHECKED BY AUTHOR)
25) **KOH:** KAPLAN,A.P.,HOOD,L.,TERRY,W.D. & METZGER,H. (1971) IMMUNOCHEMISTRY,8,801-811. (CHECKED BY AUTHOR)
26) **RIC:** KAPLAN,A.P.,HOOD,L.,TERRY,W.D. & METZGER,H. (1971) IMMUNOCHEMISTRY,8,801-811. (CHECKED BY AUTHOR)
27) **WIS:** FRANKLIN,E.C.,PRELLI,F. & FRANGIONE,B. (1979) PROC.NAT.ACAD.SCI.USA,76,452-456. (CHECKED BY AUTHOR 07/18/79)
28) **VAU:** FRANKLIN,E.C.,KYLE,R.,SELIGMANN,M. & FRANGIONE,B. (1979) MOL.IMMUNOL.,16,919-921. (CHECKED BY AUTHOR 12/10/82)
29) **LEB:** FRANKLIN,E.C.,KYLE,R.,SELIGMANN,M. & FRANGIONE,B. (1979) MOL.IMMUNOL.,16,919-921. (CHECKED BY AUTHOR 12/10/82)
30) **SAC:** PARR,D.M. (1981) MOL.IMMUNOL.,18,257-259. (CHECKED BY AUTHOR 03/02/82)
31) **DEE:** FRANGIONE,B. & MILSTEIN,C. (1967) NATURE,216,939-941. (CHECKED BY AUTHOR)
32) **LEA:** FRANGIONE,B. & FRANKLIN,E.C. (1977) PROG.IMMUNOL.,3,278-288. (CHECKED BY AUTHOR 07/18/79)
33) **HAR:** FRANGIONE,B. & FRANKLIN,E.C. (1977) PROG.IMMUNOL.,3,278-288. (CHECKED BY AUTHOR 07/18/79)
34) **HUS:** WANG,A.C. & FUDENBERG,H.H. (1975) ARCH.BIOCHEM.BIOPHYS.,168,657-664. (CHECKED BY AUTHOR 09/23/77)

NOTES: HUMAN HEAVY CHAINS SUBGROUP I

IDENTICAL SETS OF FRAMEWORK SEGMENTS:

FR1: SET 1: VAU[28],LEB[29]. (2 IDENTICAL)

FR2: SET 1: EU[1],HG3'CL[3]. (2 IDENTICAL)
SET 2: WOL[4]. (IDENTICAL TO 2 HUMAN V-H-III: TIL[4],TEI[10].)

FR3: SET 1: ND'CL[6]. (IDENTICAL TO 1 HUMAN V-H-III: U266'CL[106].)

FR4: SET 1: WOL[4]. (IDENTICAL TO 2 HUMAN V-H-II: MCE'[4],NZU[15]; 4 HUMAN V-H-III: TIL[4],DOB[31],WEA[33],NIE[34]; AND 1 MOUSE V-H-IIIA: MOPC47A[48].)
SET 2: ND'CL[6]. (IDENTICAL TO 1 HUMAN V-H-II: HIG1'CL[10]; 1 HUMAN V-H-III: U266'CL[106]; AND 1 MOUSE V-H-IIA: HDEX12[15].)

IDENTICAL SETS OF COMPLEMENTARITY DETERMINING REGIONS:

CDR1:

CDR2:

CDR3: SET 1: HG3'CL[3]. (IDENTICAL TO 1 HUMAN V-H-III: LAMBDA-VH26'CL[2]; 1 MOUSE V-H-IB: PJ14'CL[22]; AND 5 MOUSE V-H-IIB: 186-2'CL[3], 186-1'CL[5],102'CL[15],23'CL[18],3'CL[26].)
SET 2: ND'CL[6]. (IDENTICAL TO 1 HUMAN V-H-III: U266'CL[106].)

IDENTICAL SETS OF J-MINIGENES:

SET 1: ND'CL[6]. (IDENTICAL TO 1 HUMAN V-H-II: HIG1'CL[10]; AND 1 HUMAN V-H-III: U266'CL[106].)

NOTES: HUMAN HEAVY CHAINS SUBGROUP I (cont'd)

SPECIFIC NOTES:

3) **HG3'CL:** THE AMINO ACID SEQUENCE IS OBTAINED BY TRANSLATING THE NUCLEOTIDE SEQUENCE OF A CLONE OF HUMAN FETAL LIVER GENOMIC DNA.

6) **ND'CL:** THE AMINO ACID SEQUENCE IS OBTAINED BY TRANSLATING THE NUCLEOTIDE SEQUENCE OF A CLONE OF MOUSE CDNA. IT CORRESPONDS TO THE AMINO ACID SEQUENCE DETERMINED EARLIER EXCEPT THAT THE AMINO ACID SEQUENCE DETERMINATION GAVE PCA AT POSITION 1, VAL AT 2, VAL AT 34, GLY AT 35, ILE AT 48 AND HIS AT 49.

7) **MOT:** PAPAIN CLEAVES BETWEEN ARG 56 AND THR 57, AND BETWEEN ARG 62 AND SER 63.

12) **ZUC:** IT WAS FROM A CASE OF HEAVY CHAIN DISEASE.

14) **BOT:** IT WAS FROM A CASE OF IGM HEAVY CHAIN DISEASE.

15) **OMM'CL:** THE AMINO ACID SEQUENCE IS OBTAINED BY TRANSLATING THE NUCLEOTIDE SEQUENCE OF A CLONE OF HUMAN CELL LINE CDNA. IT WAS FROM A CASE OF HEAVY CHAIN DISEASE.

27) **WIS:** IT WAS FROM A CASE OF HEAVY CHAIN DISEASE. ITS RESIDUES AT POSITIONS 108 AND 109 ARE ASN AND CYS RESPECTIVELY, WHICH DO NOT CORRESPOND TO THE USUAL RESIDUES FOUND AT THESE POSITIONS IN HUMAN HEAVY CHAIN SUBGROUP I.

28) **VAU:** IT WAS FROM A CASE OF HEAVY CHAIN DISEASE.

29) **LEB:** IT WAS FROM A CASE OF HEAVY CHAIN DISEASE.

30) **SAC:** IT WAS FROM A CASE OF HEAVY CHAIN DISEASE.

+ THE FOLLOWING WERE EQUALLY AND MOST FREQUENTLY OCCURRING:

AT POSITION	RESIDUES
16	(ALA,SER)
19	(LYS,ARG)
33	(TYR,ALA)
43	(LYS,ARG,GLN)
50	(TRP,ILE,VAL,SER,GLY,GLU,GLN)
54	(PHE,SER)
56	(PRO,GLY)
62	(LYS,ARG)
69	(VAL,MET)
71	(LEU,ARG)
73	(PRO,THR)
75	(PHE,THR)
95	(GLY,GLU)
100D	(TYR,PRO,SER,ASN)
100E	(PHE,GLY)
100F	(THR,ASP)
100G	(TYR,SER)
100H	(LEU,SER)
100K	(TYR,PHE,LEU)
101	(PRO,ASP)

HUMAN HEAVY CHAINS SUBGROUP II

		INVARIANT RESIDUES	1 COR	2 DAW	3 OU	4 MCE #	5 CE-1 CL #	6 HE	7 SUP-T1 VH-JA CL #	8* NEWM	9 WAH	10 HIG1 CL	11 CAR	12 SA	13 IO	14 SPA #	15 NZU #	16 ERI	# OF SEQUENCES	# OF AMINO ACIDS	OCCURRENCES OF MOST COMMON AMINO ACID
	0		---	---	---	---	---	---	---	---	---	---			---	---					
	1		PCA	PCA	PCA	PCA	gln	PCA	gln	PCA	arg	gln			PCA	PCA			12	3	8(PCA)
	2		VAL	VAL	VAL	ile	VAL	VAL	VAL	VAL	leu	VAL			VAL	glu			12	4	9(VAL)
	3		THR	THR	THR	THR	asn	THR	gln	gln	gln	gln			THR	glu			12	4	6(THR)
	4		LEU	LEU	LEU	LEU	LEU	LEU	LEU	LEU	LEU	LEU			LEU	val			12	2	11(LEU)
	5		ARG	ARG	thr	lys	ARG	lys	gln	glx	gln	gln				ARG			11	4 : 5	4(+) : 4(ARG)
	6		GLU	GLU	GLU	GLU	GLU	GLU	GLU	GLX	GLU	gln				GLU			11	2	10(GLU) : 9(GLU)
	7		SER	SER	SER	SER	SER	asn	SER	SER	SER	trp				SER			11	3	9(SER)
	8	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY				---			10	1	10(GLY)
	9		PRO	PRO	PRO	PRO	PRO	PRO	PRO	PRO	PRO	ala				---			10	2	9(PRO)
	10		ALA	ALA	ALA	thr	ALA	thr	gly	gly	gly	gly				---			10	3	4(+)
	11	LEU	LEU	LEU	LEU	LEU	LEU	LEU	LEU	LEU	LEU	LEU				---			10	1	10(LEU)
	12	VAL	VAL	VAL	VAL	VAL	VAL	VAL	VAL	VAL	VAL	VAL				---			10	1	10(VAL)
	13		LYS	arg	LYS	LYS	LYS	LYS	LYS	arg	LYS	LYS				---			10	2	8(LYS)
FR1	14		PRO	PRO	PRO	PRO	ala	PRO	PRO	PRO	PRO	PRO				---			10	2	9(PRO)
	15		THR	THR	lys	THR	THR	THR	ser	ser	ser	ser				---			10	3	5(THR)
	16		GLN	GLN	GLN	glu	his	glu	glu	GLN	glu	glu				---			10	3	5(GLU)
	17		THR	THR	pro	THR	THR	THR	THR	THR	THR	THR				---			10	2	9(THR)
	18	LEU	LEU	LEU	LEU	LEU	LEU	LEU	LEU	LEU	LEU	LEU				---			10	1	10(LEU)
	19		THR	THR	THR	THR	THR	THR	ser	ser	ser	ser				---			10	2	6(THR)
	20	LEU	LEU	LEU	LEU	LEU	LEU	LEU	LEU	LEU	LEU	LEU	LEU			---			11	1	11(LEU)
	21	THR	THR	THR	THR	THR	THR	THR	THR	THR	THR	THR	THR	THR		---			12	1	12(THR)
	22	CYS	CYS	CYS	CYS	CYS	CYS	CYS	CYS	CYS	CYS	CYS	CYS	CYS		---			12	1	12(CYS)
	23		THR	THR	THR	THR	THR	THR	THR	THR	ile	ala	THR	THR		---			12	3	10(THR)
	24		PHE	PHE	PHE	PHE	PHE	leu	val	val	val	val	val	val		---			12	3	6(VAL)
	25		SER	SER	SER	SER	SER	SER	SER	SER	SER	phe	SER	SER		---			12	2	11(SER)
	26	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY		---			12	1	12(GLY)
	27		PHE	PHE	PHE	PHE	leu	leu	tyr	ser	gly	gly		gly		---			11	5	4(PHE)
	28		SER	SER	SER	SER	SER	SER	SER	thr	pro	SER		SER		---			11	3	9(SER)
	29		LEU	LEU	LEU	LEU	val	LEU	ile	phe	ile	phe				---			10	4	5(LEU)
	30		SER	SER	SER	SER	asn	thr	SER	SER	arg	SER				---			10	4	7(SER)
	31		SER	GLY	THR	THR	THR	THR	SER	ASN	ARG	GLY				---			10	5	4(THR)
	32		THR	GLU	SER	SER	ARG	ASP	GLY	ASP	THR	TYR				---			10	7	2(+)
	33		GLY	THR	ARG	GLY	GLY	GLY	TYR	TYR	GLY	TYR				---			10	4	5(GLY)
CDR1	34		MET	MET	MET	VAL	MET	VAL	TYR	TYR	TYR	TRP				---			10	4	4(MET)
	35		CYS	CYS	ARG	GLY	SER	ALA	TRP	THR	TYR	SER				---			10	8	2(+)
	35A		VAL	VAL	VAL	VAL	VAL	VAL	GLY	---	TRP	---				---			8	3	6(VAL)
	35B		GLY	ALA	SER	GLY	SER	GLY	---	---	GLY	---				---			7	3	4(GLY)
	36	TRP	TRP	TRP	TRP	TRP	TRP	TRP	TRP	TRP	TRP	TRP				---			10	1	10(TRP)
	37		ILE	ILE	ILE	ILE	ILE	ILE	ILE	VAL	ILE	ILE				---			10	2	9(ILE)
	38	ARG	ARG	ARG	ARG	ARG	ARG	ARG	ARG	ARG	ARG	ARG				---			10	1	10(ARG)
	39		GLN	GLN	ARG	GLN	GLN	GLN	GLN	GLN	GLN	GLN				---			10	2	9(GLN)
	40		PRO	PRO	PRO	ARG	PRO	GLY	PRO	PRO	PRO	PRO				---			10	3	8(PRO)
	41	PRO	PRO	PRO	PRO	PRO	PRO	PRO	PRO	PRO	PRO	PRO				---			10	1	10(PRO)
FR2	42	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY				---			10	1	10(GLY)
	43		LYS	GLU	LYS	LYS	LYS	ARG	LYS	ARG	LYS	ARG				---			10	3	6(LYS)
	44		GLY	ALA	ALA	ALA	ALA	ALA	GLY	GLY	GLY	GLY				---			10	2	5(+)
	45	LEU	LEU	LEU	LEU	LEU	LEU	LEU	LEU	LEU	LEU	LEU				---			10	1	10(LEU)
	46	GLU	GLU	GLU	GLU	GLU	GLU	GLU	GLU	GLU	GLU	GLU				---			10	1	10(GLU)
	47	TRP	TRP	TRP	TRP	TRP	TRP	TRP	TRP	TRP	TRP	TRP				---			10	1	10(TRP)
	48		LEU	LEU	LEU	LEU	LEU	LEU	ILE	ILE	ILE	ILE				---			10	2	6(LEU)
	49		ALA	ALA	ALA	ALA	ALA	ALA	GLY	GLY	GLY	GLY				---			10	2	6(ALA)
	50		ARG	TRP	ARG	PHE	ARG	TRP	SER	TYR	GLY	GLU				---			10	7	3(ARG)
	51		ILE	ASP	ILE	ILE	ILE	LEU	ILE	VAL	VAL	ILE				---			10	4	6(ILE)
	52		ASP	ILE	ASX	ASN	ASP	LEU	TYR	PHE	TYR	ASN				---			10	6	3(ASN) : 3(ASP)
	52A		---	---	---	---	---	TYR	HIS	---	---	---				---			2	2	1(+)
	52B		---	---	---	---	---	---	---	---	---	---				---					
	52C		---	---	---	---	---	---	---	---	---	---				---					
	53		TRP	LEU	ASX	TRP	TRP	TRP	---	TYR	TYR	HIS				---			9	5	4(TRP)
	54		ASP	ASN	ASX	ASP	ASP	ASP	SER	HIS	THR	SER				---			10	5	5(ASP) : 4(ASP)
	55		ASP	ASP	ASP	ASP	ASP	ASP	GLY	GLY	GLY	GLY				---			10	2	6(ASP)
	56		ASP	ASP	LYS	ASP	ASP	ASP	SER	THR	SER	SER				---			10	4	5(ASP)
	57		LYS	LYS	PHE	ASN	LYS	LYS	THR	SER	ILE	THR				---			10	6	4(LYS)
	58		TYR	TYR	TYR	ARG	TYR	ARG	TYR	ASP	TYR	ASN				---			10	4	6(TYR)
CDR2	59		TYR	TYR	TRP	TYR	TYR	PHE	TYR	ASP	TYR	TYR				---			10	4	7(TYR)
	60		ASX	GLY	SER	SER	GLY	SER	ASN	THR	ASN	LYS				---			10	5 : 6	3(+) : 3(SER)
	61		THR	ALA	THR	PRO	THR	PRO	PRO	THR	PRO	THR				---			10	3	5(THR)
	62		SER	SER	SER	SER	SER	SER	SER	PRO	SER	SER				---			10	2	9(SER)
	63	LEU	LEU	LEU	LEU	LEU	LEU	LEU	LEU	LEU	LEU	LEU				---			10	1	10(LEU)
	64		GLU	GLU	ARG	ARG	GLU	LYS	LYS	ARG	ARG	LYS				---			10	3	4(ARG)
	65		THR	THR	THR	SER	THR	SER	SER	SER	GLY	SER				---			10	3	5(SER)
	66	ARG	ARG	ARG	ARG	ARG	ARG	ARG	ARG	ARG	ARG	ARG				---			10	1	10(ARG)
	67		LEU	LEU	LEU	LEU	LEU	LEU	VAL	VAL	VAL	VAL				---			10	2	6(LEU)
	68		THR	ALA	SER	THR	THR	THR	THR	THR	THR	THR				---			10	3	8(THR)
	69		ILE	VAL	ILE	GLY	ILE	VAL	ILE	MET	ILE	ILE				---			10	4	6(ILE)
	70		SER	SER	SER	THR	SER	THR	SER	LEU	SER	SER				---			10	3	7(SER)
	71		LYS	LYS	LYS	LYS	LYS	ARG	VAL	VAL	VAL	LEU				---			10	4	5(LYS)
	72		ASP	ASP	ASN	ASP	ASP	ASP	ASP	ASP	ASP	ASP				---			10	2	9(ASP)
	73		THR	THR	ASP	THR	THR	THR	THR	THR	THR	THR				---			10	2	9(THR)
	74	SER	SER	SER	SER	SER	SER	SER	SER	SER	SER	SER				---			10	1	10(SER)
	75		ARG	LYS	LYS	ARG	LYS	LYS	LYS	LYS	ARG	LYS				---			10	2	7(LYS)
	76	ASN	ASN	ASN	ASN	ASN	ASN	ASN	ASN	ASN	ASN	ASN				---			10	1	10(ASN)
	77		GLN	GLN	GLN	GLN	GLN	GLN	GLN	GLN	GLN	LEU				---			10	2	9(GLN)
	78		VAL	VAL	VAL	VAL	VAL	VAL	PHE	PHE	PHE	PHE				---			10	2	6(VAL)
	79		VAL	VAL	VAL	VAL	VAL	VAL	SER	SER	SER	SER				---			10	2	6(VAL)
	80	LEU	LEU	LEU	LEU	LEU	LEU	LEU	LEU	LEU	LEU	LEU				---			10	1	10(LEU)
	81		THR	SER	ILE	THR	LYS	THR	LYS	ARG	ASN	LYS				---			10	6	3(+)
	82		MET	MET	MET	ILE	VAL	MET	LEU	LEU	LEU	LEU				---			10	4	4(+)
	82A		---	ASN	ILE	THR	THR	THR	SER	SER	ARG	SER				---			9	5	3(+)
	82B		---	THR	ASN	ASN	ASN	ASN	SER	SER	SER	SER				---			9	3	4(+)
	82C		---	VAL	VAL	MET	MET	MET	VAL	VAL	MET	VAL				---	MET		10	2	5(+)
	83		ASP	GLY	ASN	ASP	ASP	ASP	THR	THR	SER	THR				---	ASP		11	5	5(ASP)
	84		PRO	PRO	PRO	PRO	PRO	PRO	ALA	ALA	ALA	ALA				---	PRO		11	2	7(PRO)
	85		VAL	GLY	VAL	VAL	ALA	VAL	ALA	ALA	ALA	ALA				---	VAL		11	3	5(+)
	86	ASP	ASP	ASP	ASP	ASP	ASP	ASP	ASP	ASP	ASP	ASP				---	ASP		11	1	11(ASP)
	87		THR	THR	THR	SER	THR	THR	THR	THR	THR	THR				---	SER		11	2	9(THR)
	88		ALA	ALA	ALA	GLY	ALA	ALA	ALA	ALA	ALA	ALA				---	GLY		11	2	9(ALA)
	89		THR	THR	THR	THR	THR	THR	VAL	VAL	MET	VAL				---	THR		11	3	7(THR)
	90	TYR	TYR	TYR	TYR	TYR	TYR	TYR	TYR	TYR	TYR	TYR				---	TYR		11	1	11(TYR)
	91		TYR	TYR	TYR	PHE	TYR	TYR	TYR	TYR	TYR	TYR				---	PHE		11	2	9(TYR)
	92	CYS	CYS	CYS	CYS	CYS	CYS	CYS	CYS	CYS	CYS	CYS				---	CYS		11	1	11(CYS)
	93		ALA	ALA	ALA	ALA	ALA	VAL	ALA	ALA	ALA	ALA				---	ALA		11	2	10(ALA)
	94		ARG	ARG	ARG	HIS	ARG	HIS	ARG	ARG	ARG	ARG				---	HIS		11	2	8(ARG)
	95		ILE	SER	VAL	ARG	MET	ARG	VAL	ASN	GLY	GLY				---	ARG		11	7	3(ARG)
	96		THR	CYS	VAL	PRO	GLN	HIS	ARG	LEU	ASN	LEU				---	PRO		11	9	2(+)
	97		VAL	GLY	ASN	PRO	VAL	PRO	ARG	ILE	PRO	LEU				---	PRO		11	7	4(PRO)
	98		ILE	SER	SER	TRP	THR	ARG	ARG	ALA	PRO	ARG				---	TRP		11	7	3(ARG)
	99		PRO	GLN	VAL	ARG	MET	THR	---	GLY	PRO	GLY				---	ARG		10	7	2(+)
	100		ALA	TYR	MET	PHE	VAL	LEU	---	CYS	TYR	GLY				---	PHE		10	8	2(+)
	100A		PRO	PHE	ALA	THR	ARG	ALA	---	ILE	TYR	TRP				---	THR		10	8	2(+)
	100B		ALA	---	GLY	GLY	GLU	---	---	---	ASP	ASN				---	SER		7	6	2(GLY)
	100C		GLY	---	TYR	ASN	VAL	---	---	---	ILE	ASP				---	ASP		7	6	2(ASP)
	100D		TYR	---	TYR	LEU	MET	---	---	---	GLY	VAL				---	LEU		7	5	2(+)
	100E		---	---	TYR	GLY	ILE	---	---	---	THR	ASP				---	GLY		6	5	2(GLY)
CDR3	100F		---	---	TYR	GLY	THR	---	---	---	GLY	TYR				---	SER		6	4	2(+)
	100G		---	---	TYR	---	SER	---	TYR	---	SER	TYR				---	---		5	2	3(TYR)
	100H		---	---	---	---	ASN	---	SER	---	ASP	TYR				---	---		4	4	1(+)
	100I		---	---	---	---	---	---	SER	---	ASP	GLY				---	---		3	3	1(+)
	100J		---	---	---	---	ALA	---	ALA	---	GLY	MET				---	---		4	3	2(ALA)
	100K		MET	---	MET	PHE	PHE	PHE	SER	---	ILE	---				---	PHE		8	4	4(PHE)
	101		ASP	ASP	ASP	ASP	ASP	ASP	LYS	ASP	ASP	ASP				---	SER	ASP	12	3	10(ASP)
	102		VAL	TYR	VAL		ILE	VAL	ILE	VAL	VAL	VAL				---	PRO	VAL	11	4	7(VAL)
	103		TRP	TRP	TRP	TRP	TRP	TRP	ILE	TRP	TRP	TRP				---	TRP	TRP	12	2	11(TRP)
	104		GLY	GLY	GLY	GLY	GLY	GLY	PHE	GLY	GLY	GLY				---	GLY	GLY	12	2	11(GLY)
	105		ARG	GLN	LYS	GLN	GLN	GLN	GLY	GLN	GLN	GLN				---	GLN	ARG	12	4	8(GLN)
	106		GLY	GLY	GLY	GLY	GLY	GLY	SER	GLY	GLY	GLY				---	GLY	GLY	12	2	11(GLY)
FR4	107		THR	ILE	THR	THR	THR	THR	GLY	SER	THR	THR				---	THR	THR	12	4	9(THR)
	108		PRO	LEU	THR	LEU	MET	LYS	THR	LEU	THR	THR				---	LEU	THR	12	5	5(THR)
	109		VAL	VAL	VAL	VAL	VAL	VAL	ARG	VAL	VAL	VAL				---	VAL	VAL	12	2	11(VAL)
	110		THR	THR	THR	THR	THR	ALA	LEU	THR	HIS	THR				---	THR	THR	12	4	9(THR)
	111		VAL	VAL	VAL	VAL	VAL	VAL	SER	VAL	VAL	VAL				---	VAL	VAL	12	2	11(VAL)
	112		SER	SER	SER	SER	SER	SER	ILE	SER	SER	SER				---	SER	SER	12	2	11(SER)
	113					SER	SER		ARG	SER	SER	SER				---	SER	ALA	8	3	6(SER)

HUMAN HEAVY CHAINS SUBGROUP II (cont'd)

VARIABILITY

	0	
	1	4.5
	2	5.3
	3	8.
	4	2.2
	5	11. : 14.
	6	2.2 : 2.4
	7	3.7
	8	1.
	9	2.2
	10	7.5
	11	1.
	12	1.
	13	2.5
	14	2.2
FR1	15	6.
	16	6.
	17	2.2
	18	1.
	19	3.3
	20	1.
	21	1.
	22	1.
	23	3.6
	24	6.
	25	2.2
	26	1.
	27	14.
	28	3.7
	29	8.
	30	5.7
	31	13.
	32	35.
CDR1	33	8.
	34	10.
	35	40.
	35A	
	35B	
	36	1.
	37	2.2
	38	1.
	39	2.2
	40	3.8
	41	1.
FR2	42	1.
	43	5.
	44	4.
	45	1.
	46	1.
	47	1.
	48	3.3
	49	3.3
	50	23.
	51	6.7
	52	20.
	52A	
	52B	
	52C	
	53	11.
	54	10. : 13.
	55	3.3
	56	8.
CDR2	57	15.
	58	6.7
	59	5.7
	60	17. : 20.
	61	6.
	62	2.2
	63	1.
	64	7.5
	65	6.
	66	1.
	67	3.3
	68	3.8
	69	6.7
	70	4.3
	71	8.
	72	2.2
	73	2.2
	74	1.
	75	2.9
	76	1.
	77	2.2
	78	3.3
	79	3.3
	80	1.
FR3	81	20.
	82	10.
	82A	
	82B	
	82C	
	83	11.
	84	3.1
	85	6.6
	86	1.
	87	2.4
	88	2.4
	89	4.7
	90	1.
	91	2.4
	92	1.
	93	2.2
	94	2.8
	95	26.
	96	50.
	97	19.
	98	26.
	99	35.
	100	40.
	100A	
	100B	
	100C	
CDR3	100D	
	100E	
	100F	
	100G	
	100H	
	100I	
	100J	
	100K	
	101	3.6
	102	6.3
	103	2.2
	104	2.2
	105	6.
	106	2.2
	107	5.3
FR4	108	12.
	109	2.2
	110	5.3
	111	2.2
	112	2.2
	113	4.

ANTIBODY SPECIFICITIES: HUMAN HEAVY CHA[redacted]UBGROUP II

8) **NEWM:** ANTI-3-(3'-HYDROXY-3',7',11',15',TETRAMETHYL HEXADECYL) 2-METHYL 1,4 NAPHTHOQUINONE(VIT.K1OH)

CLASS: HUMAN HEAVY CHAINS SUBGROUP II

1) **COR:** IGG1-
2) **DAW:** IGG1-LAMBDA
3) **OU:** IGM-KAPPA
4) **MCE':** IGM-KAPPA
6) **HE:** IGG1-
8) **NEWM:** IGG1-LAMBDA
9) **WAH:** IGD-LAMBDA
12) **SA:** IGG2-LAMBDA
15) **NZU:** IGM-
16) **ERI:** IGD-

REFERENCE: HUMAN HEAVY CHAINS SUBGROUP II

1) **COR:** PRESS,E.M. & HOGG,N.M. (1970) BIOCHEM.J.,117,641-660. (CHECKED BY AUTHOR)
2) **DAW:** PRESS,E.M. & HOGG,N.M. (1970) BIOCHEM.J.,117,641-660. (CHECKED BY AUTHOR)
3) **OU:** PUTNAM,F.W.,SHIMIZU,A.,PAUL.,C.,SHINODA,T. & KOHLER,H. (1971) ANN.N.Y.ACAD.SCI.,190,83-103. (CHECKED BY AUTHOR 06/15/83)
4) **MCE':** GERBER-JENSON,B.,KAZIN,A.,KEHOE,J.M.,SCHEFFEL,C.,ERICKSON,B.W. & LITMAN,G.W. (1981) J.IMMUNOL.,126,1212-1216. (CHECKED BY AUTHOR 12/15/80)
5) **CE-1 'CL:** TAKAHASHI,N.,NOMA,T. & HONJO,T. (1984) PROC.NAT.ACAD.SCI.USA,81,5194-5198.
6) **HE:** CUNNINGHAM,B.A.,GOTTLIEB,P.D.,PFLUMM,M.N. & EDELMAN,G.M. (1971) PROGRESS IN IMMUNOLOGY (B.AMOS,ED.),ACADEMIC PRESS,N.Y.,PP.3-24. (CHECKED BY AUTHOR)
7) **SUP-T1 VH-JA'CL:** DENNY,C.T.,YOSHIKAI,Y.,MAK,T.W.,SMITH,S.D.,HOLLIS,G.F. & KIRSCH,I.R. (1986) NATURE,320,549-551.
8) **NEWM:** POLJAK,R.J.,AMZEL,L.M.,CHEN,B.L.,PHIZACKERLEY, R.P. & SAUL,F. (1974) PROC.NAT.ACAD.SCI.USA,71,3440-3444. (CHECKED BY AUTHOR WHO CORRECTED RESIDUES 6,9,15,16,24,26,27,29 THROUGH 35B,59,60 AS GIVEN IN TABLE OF THE FIRST EDITION OF THIS BOOK, AND HAS MORE RECENTLY REVISED RESIDUES 5,24,28,29,30,31,33,34,35,35A,35B,59,60 AND 101); POLJAK,R.J.,AMZEL,L.M.,CHEN,B.L.,CHIU,Y.Y., PHIZACKERLEY,R.P.,SAUL,F. & YSERN,X. (1976) COLD SPRING HARBOR SYMP. QUANTITATIVE BIOL.,41,639-645; POLJAK,R.J.,NAKASHIMA,Y.,CHEN, B.L. & KONIGSBERG,W. (1977) BIOCHEMISTRY,16,3412-3420. THE SEQUENCE LISTED IN THE LAST REFERENCE IS GIVEN IN THE TABLE. (CHECKED BY AUTHOR, W.K., 09/30/78)
9) **WAH:** PUTNAM,F.W.,TAKAHASHI,N.,TETAERT,D.,DEBUIRE,B. & LIN,L.C. (1981) PROC.NAT.ACAD.SCI.USA,78,6168-6172. (CHECKED BY AUTHOR 11/30/81); TAKAHASHI,N.,TETAERT,D.,DEBUIRE,B.,LIN,L. & PUTNAM,F.W. (1982) PROC.NAT.ACAD.SCI.USA,79,2650-2654.
10) **HIG1'CL:** KUDO,A.,ISHIHARA,T.,NISHIMURA,Y. & WATANABE,T. (1985) GENE,33,181-189. (CHECKED BY AUTHOR 10/01/85)
11) **CAR:** FRANGIONE,B. (1968) PH.D. THESIS, UNIVERSITY OF CAMBRIDGE. (CHECKED BY AUTHOR)
12) **SA:** MILSTEIN,C. & FRANGIONE,B. (1971) BIOCHEM.J.,121,217-225. (CHECKED BY AUTHOR)
13) **IO:** MONTGOMERY,P.C.,BELLO,A.C. & ROCKEY,J.H. (1970) BIOCHIM.BIOPHYS.ACTA,200,258-266. (CHECKED BY AUTHOR)
14) **SPA:** FRANGIONE,B. & FRANKLIN,E.C. (1979) J.IMMUNOL.,122,1177-1179. (CHECKED BY AUTHOR 07/18/79)
15) **NZU:** ERICKSON,B.W.,GERBER-JENSON,B.,WANG,A.C. & LITMAN,G.W. (1981) MOL.IMMUNOL.,19,357-365. (CHECKED BY AUTHOR 11/30/81)
16) **ERI:** MILSTEIN,C.P. & DEVERSON,E.V. (1980) IMMUNOLOGY,40,657-664. (CHECKED BY AUTHOR 11/30/82)

NOTES: HUMAN HEAVY CHAINS SUBGROUP II

IDENTICAL SETS OF FRAMEWORK SEGMENTS:

FR1:
FR2: SET 1: SUP-T1 VH-JA'CL[7],WAH[9]. (2 IDENTICAL)
FR3:
FR4: SET 1: MCE'[4],NZU[15]. (2 IDENTICAL HUMAN V-H-II; ALSO 1 HUMAN V-H-I: WOL[4]; 4 HUMAN V-H-III: TIL[4],DOB[31],WEA[33],NIE[34]; AND 1 MOUSE V-H-IIIA: MOPC47A[48].)
SET 2: HIG1'CL[10]. (IDENTICAL TO 1 HUMAN V-H-I: ND'CL[6]; 1 HUMAN V-H-III: U266'CL[106]; AND 1 MOUSE V-H-IIA: HDEX12[15].)

IDENTICAL SETS OF J-MINIGENES:

SET 1: HIG1'CL[10]. (IDENTICAL TO 1 HUMAN V-H-I: ND'CL[6]; AND 1 HUMAN V-H-III: U266'CL[106].)

SPECIFIC NOTES:

4) **MCE':** IT IS A CRYOIMMUNOGLOBULIN AND IS DESIGNATED BY THE AUTHORS AS MCE. IN ORDER TO DIFFERENTIATE IT FROM ANOTHER MCE SEQUENCED BY CAPRA ET AL., IT IS DENOTED AS MCE'.
5) **CE-1 'CL:** CELL LINE CESS
7) **SUP-T1 VH-JA'CL:** IT IS FROM A PATIENT SUFFERING FROM CHILDHOOD T-CELL LYMPHOMA WITH inv(14)(q11.2;q32.2). THE INVERSION ON CHROMOSOME 14 BRINGS THE VH GENE AND JA MINIGENE TOGETHER, GIVING RISE TO A HYBRID MOLECULE CONTAINING PART OF THE IMMUNOGLOBULIN GENE AND PART OF THE T-LYMPHOCYTE RECEPTOR FOR ANTIGEN GENE.
14) **SPA:** IT WAS FROM A CASE OF HEAVY CHAIN DISEASE.
15) **NZU:** IT IS A CRYOIMMUNOGLOBULIN.

\+ THE FOLLOWING WERE EQUALLY AND MOST FREQUENTLY OCCURRING:

AT POSITION	RESIDUES
5	(ARG,GLN)
10	(ALA,GLY)
32	(THR,SER,ASP)
35	(CYS,SER)
44	(ALA,GLY)
52A	(TYR,HIS)
60	(SER,ASN)
81	(LYS,THR)
82	(LEU,MET)
82A	(THR,SER)
82B	(SER,ASN)
82C	(VAL,MET)
85	(VAL,ALA)
96	(PRO,LEU)
99	(PRO,ARG,GLY)
100	(TYR,PHE)
100A	(ALA,THR)
100D	(TYR,LEU)
100F	(TYR,GLY)
100H	(TYR,SER,ASP,ASN)
100I	(SER,GLY,ASP)

HUMAN HEAVY CHAINS SUBGROUP III

		INVARIANT RESIDUES	1* TUR	2 LAMBDA -VH26 'CL #	3* POM	4 TIL	5 WAS	6 HF2-1/13B	7 HF2-1/17	8 HF2-18/2	9 H11 'CL	10 TEI	11 BRO 'IGM	12 GR'	13 WAT	14* LAY	15 GRA' #	16* FR #	17 MU	18 VIN	19 HF3-16/6	20 BEN (III)	21 ZAP	22 JON	23 KEA
	0		---	#	---	---	---	---	---	---	---	---	---	---	---	---	---	---	---	---	---	---	---	---	---
	1		GLU	GLU	GLU	GLU	GLU	GLU	GLU	GLU	GLU	GLU	GLU	GLU	GLU	ala	GLU	GLU	GLU	GLU	GLU	GLU	GLU	asp	GLU
	2		VAL	VAL	VAL	VAL	VAL	VAL	VAL	VAL	VAL	VAL	VAL	VAL	VAL	VAL	VAL	VAL	VAL	VAL	VAL	VAL	VAL	VAL	VAL
	3		GLN	GLN	GLN	GLN	GLN	GLN	GLN	GLN	GLN	GLN	GLN	GLN	GLN	GLN	GLN	GLN	GLN	GLN	GLN	GLN	GLN	GLN	GLN
	4	LEU(.97)	LEU	LEU	LEU	LEU	LEU	LEU	LEU	LEU	LEU	LEU	LEU	LEU	LEU	LEU	LEU	LEU	LEU	LEU	LEU	LEU	LEU	LEU	LEU
	5		LEU	LEU	LEU	LEU	LEU	LEU	LEU	LEU	val	val	val	val	val	LEU	val	val	val	val	LEU	val	val	val	val
	6		GLU	GLU	GLU	GLU	GLU	GLU	GLU	gln	GLU	GLU	GLU	GLU	GLU	GLU	GLU	asp	GLU	GLU	gln	GLU	GLU	GLU	GLX
	7	SER(.97)	SER	SER	SER	SER	SER	SER	SER	SER	SER	SER	SER	SER	SER	SER	SER	SER	SER	SER	SER	SER	SER	SER	SER
	8	GLY(.99)	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY
	9	GLY(.98)	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY
	10		GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	ala	GLY	GLY
	11		LEU	LEU	LEU	LEU	LEU	LEU	LEU	LEU	LEU	LEU	LEU	LEU	LEU	LEU	LEU	LEU	LEU	LEU	LEU	LEU	LEU	LEU	LEU
	12		VAL	VAL	VAL	VAL	VAL	VAL	VAL	VAL	VAL	VAL	VAL	VAL	VAL	VAL	VAL	VAL	VAL	ile	VAL	ala	VAL	VAL	VAL
	13		GLN	GLN	GLN	GLN	GLN	GLN	GLN	GLN	GLN	GLN	GLN	GLN	GLN	GLN	GLN	GLN	lys	GLN	GLN	GLN	GLN	lys	lys
FR 1	14	PRO(.95)	PRO	PRO	PRO	PRO	PRO	PRO	PRO	PRO	PRO	PRO	PRO	PRO	PRO	PRO	PRO	PRO	PRO	PRO	PRO	PRO	PRO	PRO	PRO
	15	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY
	16		GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY
	17	SER(.97)	SER	SER	SER	SER	SER	SER	SER	SER	SER	SER	SER	SER	SER	SER	SER	SER	SER	SER	SER	SER	SER	SER	SER
	18	LEU(.97)	LEU	LEU	LEU	LEU	LEU	LEU	LEU	LEU	LEU	LEU	LEU	LEU	LEU	LEU	LEU	LEU	LEU	LEU	LEU	LEU	gly	LEU	LEU
	19		ARG	ARG	ARG	ARG	ARG	ARG	ARG	ARG	ARG	ARG	ARG	ARG	ARG	ARG	ARG	ARG	ARG	ARG	ARG	ARG	ARG	ARG	ARG
	20		LEU	LEU	LEU	LEU	LEU	LEU	LEU	LEU	LEU	LEU	LEU	LEU	LEU	LEU	LEU	LEU	LEU	LEU	LEU	LEU	LEU	LEU	LEU
	21		SER	SER	SER	SER	SER	SER	SER	SER	SER	SER	SER	SER	SER	SER	SER	SER	SER	SER	gln	ala	SER	SER	SER
	22	CYS	CYS	CYS	CYS	CYS	CYS	CYS	CYS	CYS	CYS	CYS	CYS	CYS	CYS	CYS	CYS	CYS	CYS	CYS	CYS	CYS	CYS	CYS	CYS
	23		ALA	ALA	ALA	ALA	ALA	ALA	ALA	ALA	ALA	ALA	ALA	ALA	ALA	ALA	ALA	ALA	ALA	ALA	ALA	ALA	ALA	ALA	ALA
	24		ALA	ALA	ALA	ALA	ALA	ALA	ALA	ALA	ALA	ALA	ALA	ALA	ALA	ALA	ALA	ALA	ALA	ALA	ALA	ALA	ALA	ALA	ALA
	25	SER(.98)	SER	SER	SER	SER	SER	SER	SER	SER	SER	SER	SER	SER	SER	SER	SER	SER	SER	SER	SER	SER	SER	SER	SER
	26	GLY(.97)	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	SER	GLY	GLY	GLY
	27	PHE(.98)	PHE	PHE	PHE	PHE	PHE	PHE	PHE	PHE	PHE	PHE	PHE	PHE	PHE	PHE	PHE	PHE	PHE	PHE	PHE	PHE	PHE	PHE	PHE
	28		THR	THR	THR	THR	ser	lys	lys	THR	THR	THR	THR	THR	THR	THR	THR	THR	THR	THR	ser	THR	THR	THR	ile
	29		PHE	PHE	PHE	PHE	PHE	PHE	PHE	PHE	PHE	PHE	PHE	PHE	PHE	PHE	ile	PHE	PHE	val	PHE	PHE	PHE	PHE	PHE
	30		SER	SER	SER	SER	SER	SER	SER	SER	SER	SER	SER	SER	asx	SER	SER	SER	thr	SER	SER	SER	SER	SER	pro
	31		ARG	SER	SER	THR	THR	SER	SER	SER	SER	THR	TYR	ALA	THR	ALA	LYS	ASX	ARG	THR	PRO	THR	THR	THR	
	32		VAL	TYR	SER	TYR	ASP	TYR	TYR	TYR	TYR	SER	TYR	ASX	TYR	SER	THR	PHE	GLY	ASN	SER	THR	THR	ALA	TYR
CDR 1	33		LEU	ALA	ALA	VAL	ALA	ALA	ALA	ALA	TRP	ALA	ASN	TYR	THR	ALA	VAL	TYR	GLY	TYR	ALA	PHE	SER	TRP	
	34		SER	MET	MET	MET	MET	MET	MET	MET	MET	VAL	MET	MET	MET	MET	TYR	MET	LEU	MET	MET	MET	ARG	MET	
	35		SER	SER	SER	SER	TYR	SER	SER	SER	HIS	TYR	ASN		VAL	SER	GLU	ASP	GLU		SER	ARG	PHE	LYS	
	35A		---	---	---	---	---	---	---	---	---	---	---	---		---	---	---			---	---	---	---	
	35B		---	---	---	---	---	---	---	---	---	---	---	---		---	---	---			---	---	---	---	
	36	TRP	TRP	TRP	TRP	TRP	TRP	TRP	TRP	TRP	TRP	TRP	TRP	TRP		TRP	TRP	TRP	TRP		TRP	TRP	TRP	TRP	
	37	VAL(.95)	VAL	VAL	VAL	VAL	VAL	VAL	VAL	VAL	VAL	VAL	VAL	VAL		VAL	VAL	VAL	VAL		VAL	VAL	VAL	VAL	
	38	ARG(.97)	ARG	ARG	ARG	ARG	ARG	ARG	ARG	ARG	ARG	ARG	ARG	PRO		ARG	ARG	ARG	ARG		ARG	ARG	ARG	ARG	
	39	GLN(.97)	GLN	GLN	GLN	GLN	GLN	GLN	GLN	GLN	GLN	GLN	GLN	GLY		GLN	GLN	GLN	GLN		GLN		GLN	GLN	
	40		ALA	ALA	ALA	ALA	ALA	ALA	ALA	ALA	ALA	ALA	VAL	ALA		ALA	ALA	ALA	ALA		ALA		ALA	ALA	
	41		PRO	PRO	PRO	PRO	PRO				PRO	PRO	THR	PRO		PRO	PRO	PRO	PRO				PRO	PRO	
FR 2	42	GLY	GLY	GLY	GLY	GLY	GLY				GLY	GLY	GLY	GLY		GLY	GLY	GLY	GLY				GLY	GLY	
	43	LYS(.97)	LYS	LYS	LYS	LYS	LYS				LYS	LYS	LYS	ARG		LYS	LYS	LYS	LYS				LYS	LYS	
	44		GLY	GLY	GLY	GLY	GLY				GLY	GLY	GLY	GLY		GLY	GLY	GLY	ALA				GLY	GLY	
	45	LEU(.97)	LEU	LEU	LEU	LEU	LEU				LEU	LEU	LEU	LEU		LEU	LEU	LEU	LEU				LEU	LEU	
	46		GLU	GLU	GLU	GLX	GLU				VAL	GLU	GLU			GLU	GLU	GLU	GLX				GLU	GLU	
	47	TRP	TRP	TRP	TRP	TRP	TRP				TRP	TRP	TRP			TRP	TRP	TRP	TRP				TRP	TRP	
	48		VAL	VAL	VAL	VAL	VAL				VAL	VAL	VAL			VAL	VAL	VAL	VAL				VAL	VAL	
	49		SER	SER	ALA	GLY	ALA				SER	GLY	SER			ALA	THR	ALA	LEU				GLU	VAL	
	50		GLY	ALA	TRP	ALA	TRP				ARG	TRP	ALA			TRP	TYR	ALA	VAL				PHE	TRP	
	51		ARG	ILE	LYS	ILE	LYS				ILE	ARG	ILE			LYS	VAL	ARG	PHE				ARG	ARG	
	52		LEU	SER	TYR	GLX	TYR				ASN	TYR	GLY			TYR	GLY		SER				VAL	VAL	
	52A		ASN	GLY	GLU	GLY	GLN				SER	GLU	---			GLU	GLN		VAL				GLN	GLU	
	52B	LYS	---	---	---	---	---				---	---	---			---	---		---				---	---	
	52C		---	---	---	---	---				---	---	---			---	---		---				---	---	
	53		ALA	SER	ASN	LEU	GLU				ASP	GLY	THR			ASN	VAL		THR				GLY	GLN	
	54		SER	GLY	GLY	SER	ALA				GLY	SER	ALA			GLY	SER						SER	VAL	
	55		SER	GLY	ASN	VAL	SER				SER	SER	GLY			ASN	LYS						ALA	VAL	
	56		ASN	SER	ASP	SER	ASN				SER	LEU	ASP			ASP	PHE						ILE	GLU	
CDR 2	57		LEU	THR	LYS	GLX	SER				THR	THR	GLN			LYS	SER		LYS				SER	LYS	
	58		HIS	TYR	HIS	SER	HIS				THR	HIS	TYR			HIS			PHE				HIS	ALA	
	59		PHE	TYR	TYR	TYR	PHE				TYR	TYR	TYR			TYR	TYR		TYR				TYR	PHE	
	60		ALA	GLY	ALA	ALA	ALA				ALA	ALA	ALA			ALA	ALA		THR				ALA	ALA	
	61		VAL	ASP	ASP	ASX	ASP				ASP	VAL	ASP			ASP	VAL		GLU				ASP	ASN	
	62		SER	SER	SER	SER	THR				SER	SER	SER			SER	SER		SER				SER	SER	
	63		ALA	VAL	VAL	VAL	VAL				VAL	VAL	VAL			VAL	VAL		LEU				VAL	VAL	
	64		GLN	LYS	ASN	LYS	ASN				LYS	GLN	LYS			ASN	GLN		ASN				GLN	ASN	
	65	GLY(.97)	GLY	GLY	GLY	GLY	GLY				GLY	GLY	GLY			GLY	GLY						ALA	GLY	
	66	ARG	ARG	ARG	ARG	ARG	ARG				ARG	ARG	ARG			ARG	ARG						ARG	ARG	
	67	PHE(.97)	PHE	PHE	PHE	PHE	PHE				PHE	PHE	PHE			PHE	PHE						PHE	PHE	
	68		THR	THR	THR	THR	THR				THR	THR	THR			THR	THR						THR	THR	
	69	ILE(.97)	ILE	ILE	ILE	ILE	ILE				ILE	ILE	ILE			ILE	ILE						ILE	ILE	
	70	SER(.97)	SER	SER	SER	SER	SER				SER	SER	SER			SER	SER						SER	SER	
	71	ARG	ARG	ARG	ARG	ARG	ARG				ARG	ARG	ARG			ARG	ARG						ARG	ARG	
	72		ASN	ASP	ASN	ASP	ASN				ASP	ASN	ASN			ASN	ASN						ASN	ASN	
	73		ASP	ASN	ASP	ASP	ASP				ASN	ASP	ASP			ASP	ASP						ASP	ASP	
	74		SER	SER	SER	SER	SER				ALA	SER	SER			SER	SER						SER	SER	
	75		LYS	LYS	LYS	LYS	LYS				LYS	LYS	LYS			LYS	LYS						LYS	LYS	
	76		ASN	ASN	ASN	ASN	ASN				ASN	ASN	ASN			ASN	ASN						ASN	ASN	
	77		THR	THR	THR	THR	THR				THR	THR	THR			THR	THR						THR	THR	
	78		LEU	LEU	LEU	---	LEU				LEU	LEU	LEU			LEU	LEU						LEU	LEU	
	79		TYR	TYR	TYR	---	TYR				TYR	TYR	TYR			TYR	TYR						TYR	TYR	
	80		LEU	LEU	LEU	---	LEU				LEU	LEU	LEU			LEU	LEU						LEU	LEU	
	81		GLN	GLN	LEU	---	GLN				GLN	GLN	ASN			GLN	GLU						GLN	GLN	
FR 3	82	MET(.95)	MET	MET	MET	MET	MET				MET	MET	MET			MET	MET	MET					MET	MET	MET
	82A		LEU	ASN	ASN	ASN	ASN				ASN	LEU	ASN			ASN	LYS	ASN					ASN	ILE	ASN
	82B		SER	SER	SER	ARG					SER	SER	SER			GLY	THR	SER					THR	SER	ASN
	82C		LEU	LEU	LEU	LEU	LEU				LEU	LEU	LEU			LEU	GLY	LEU					GLY	VAL	LEU
	83		GLN	ARG	GLN	ARG	GLU				ARG	GLU	ARG			GLN	GLU	ARG					GLU	THR	ARG
	84		ALA	ALA	ALA	ALA	ALA				ALA	PRO	ALA			ALA	PRO	ALA		ALA			ALA	PRO	VAL
	85		GLU	GLU	GLU	GLU	GLU				GLU	GLU	GLU			GLU	GLU	GLX		GLU			GLU	GLU	GLX
	86		ASP	ASP	ASP	ASP	ASP				ASP	ASP	ASP			VAL	ASP	ASX		ASP			ASP	ASP	ASX
	87		THR	THR	THR	THR	THR				THR	THR	THR			SER	THR	THR		THR			THR	THR	THR
	88		ALA	ALA	ALA	ALA	ALA				ALA	ALA	ALA			ALA	ALA	ALA		ALA			ALA	ALA	ALA
	89		LEU	VAL	LEU	VAL	VAL				VAL	VAL	VAL			ILE	VAL	VAL		VAL			VAL	VAL	VAL
	90	TYR(.98)	TYR	TYR	TYR	TYR	TYR				TYR	TYR	TYR			TYR	TYR	TYR		TYR			TYR	TYR	TYR
	91	TYR(.95)	TYR	TYR	TYR	TYR	TYR				TYR	TYR	TYR			TYR	TYR	TYR		TYR			TYR	TYR	TYR
	92	CYS	CYS	CYS	CYS	CYS	CYS				CYS	CYS	CYS			CYS	CYS	CYS		CYS			CYS	CYS	CYS
	93		ALA	ALA	ALA	ALA	ALA				ALA	ALA	ALA			ALA	ALA	ALA		ALA			ALA	ALA	ALA
	94		ARG	LYS	ARG	LYS	ARG				ARG	ARG	ARG			ARG	ARG	ARG		ARG			ARG	ARG	ARG
	95		LEU	#	ASP	GLY	PHE				---	VAL	SER			ASP	HIS						THR	VAL	ASX
	96		SER	---	ALA	LYS	ARG				---	THR	PRO			ALA	ILE						ARG	VAL	ARG
	97		VAL	---	GLY	VAL	GLN				---	PRO	VAL			GLY	TYR						PRO	VAL	LEU
	98		THR	---	PRO	SER	PRO				---	ALA	SER			PRO	VAL						GLY	SER	GLY
	99		ALA	---	TYR	ALA	PHE				---	ALA	LEU			TYR	THR						GLY	THR	PRO
	100		VAL	---	VAL	TYR	VAL				---	ALA	VAL			VAL	LEU						TYR	SER	THR
	100A		ALA	---	SER	TYR	GLN				---	SER	ASP			SER	TYR						PHE	---	ALA
CDR 3	100B		PHE	---	PRO	PHE	---				---	LEU	GLY			PRO	TYR						SER	---	CYS
	100C		---	---	THR	---	---				---	THR	TRP			THR	TYR						---	---	SER
	100D		---	---	PHE	---	---				---	---	LEU			PHE	---						---	---	VAL
	100E		---	---	---	---	---				---	---	TYR			---	---						---	---	
	100F		---	---	---	---	---				---	---	TYR			---	---						---	---	
	100G		---	---	---	---	---				---	---	TYR			---	---						---	---	
	100H		---	---	---	---	---				---	---	TYR			---	---						---	---	
	100I		---	---	---	---	---				---	---	GLY			---	---						---	---	
	100J		---	---	---	---	PHE				---	PHE	---			---	PHE						---	MET	
	100K		---	---	PHE	---	PHE				---	SER	---			PHE	MET						---		
	101		ASP	---	ALA	ASX	ASP				---	ALA	SER			ALA	ALA						ASP	ASP	
	102		VAL	---	HIS	TYR	VAL				---	VAL				HIS	VAL						VAL	VAL	
	103		TRP	---	TYR	TRP	PHE				---	TRP	TRP			TRP	TRP						TRP	TRP	
	104	GLY(.97)	GLY	---	GLY	GLY	GLY				---	GLY	GLY			GLY	GLY						GLY	GLY	
	105		GLN	---	GLN	GLX	GLN				---	GLN	GLN			GLN	GLN						GLN	GLN	
	106	GLY(.97)	GLY	---	GLY	GLY	GLY				---	GLY	GLY			GLY	GLY						GLY	GLY	
FR 4	107		THR	---	THR	THR	THR				---	THR	THR			THR	THR						THR	THR	
	108		LYS	---	LEU	LEU	LEU				---	LEU	LEU			LEU	LEU						LEU	PRO	
	109	VAL(.97)	VAL	---	VAL	VAL	VAL				---	VAL				VAL							VAL	VAL	
	110		SER	---	THR	THR	THR				---	THR				THR							SER	THR	
	111			---		VAL					---														
	112	SER		---		SER					---														
	113			---		SER					---														